WEST

Generate Collection | Print

Search Results - Record(s) 1 through 10 of 11 returned.

1. Document ID: US 6388065 B1

L1: Entry 1 of 11 File: USPT May 14, 2002

US-PAT-NO: 6388065
DOCUMENT-IDENTIFIER: US 6388065 B1

TITLE: DNA for evaluating the progression potential of cervical lesions

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWMC | Draw Desc
Image

2. Document ID: US 6355438 B1

L1: Entry 2 of 11 File: USPT Mar 12, 2002

US-PAT-NO: 6355438
DOCUMENT-IDENTIFIER: US 6355438 B1

TITLE: Method for quantitating oligonucleotides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWMC | Draw Desc
Image

3. Document ID: US 6255067 B1

L1: Entry 3 of 11 File: USPT Jul 3, 2001

US-PAT-NO: 6255067
DOCUMENT-IDENTIFIER: US 6255067 B1

TITLE: cDNA encoding peptidyl-glycine alpha-amidating monooxygenase (PAM)

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWMC | Draw Desc
Image

4. Document ID: US 6001804 A

L1: Entry 4 of 11 File: USPT Dec 14, 1999

US-PAT-NO: 6001804
DOCUMENT-IDENTIFIER: US 6001804 A

TITLE: Pancreatic islet cell antigens obtained by molecular cloning

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

---

☐ 5. Document ID: US 5998697 A

L1: Entry 5 of 11 File: USPT Dec 7, 1999

US-PAT-NO: 5998697
DOCUMENT-IDENTIFIER: US 5998697 A

TITLE: Transgenic fish and vectors therefor

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

---

☐ 6. Document ID: US 5981700 A

L1: Entry 6 of 11 File: USPT Nov 9, 1999

US-PAT-NO: 5981700
DOCUMENT-IDENTIFIER: US 5981700 A

TITLE: Pancreatic islet cell antigens obtained by molecular cloning

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

---

☐ 7. Document ID: US 5955345 A

L1: Entry 7 of 11 File: USPT Sep 21, 1999

US-PAT-NO: 5955345
DOCUMENT-IDENTIFIER: US 5955345 A

TITLE: Nucleic acids encoding pancreatic islet cell antigens obtained by molecular cloning

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 8. Document ID: US 5840836 A

L1: Entry 8 of 11 File: USPT Nov 24, 1998

US-PAT-NO: 5840836
DOCUMENT-IDENTIFIER: US 5840836 A

TITLE: Pancreatic islet cell antigens obtained by molecular cloning

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 9. Document ID: US 5773226 A

L1: Entry 9 of 11 File: USPT Jun 30, 1998

US-PAT-NO: 5773226
DOCUMENT-IDENTIFIER: US 5773226 A

TITLE: Recombinant calf intestinal alkaline phosphatase

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 10. Document ID: US 5707853 A

L1: Entry 10 of 11 File: USPT Jan 13, 1998

US-PAT-NO: 5707853
DOCUMENT-IDENTIFIER: US 5707853 A

TITLE: Nucleic acid encoding calf intestinal alkaline phosphatase

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

Generate Collection | Print

Term	Documents
POLY-A.USPT.	1384
POLY-AS.USPT.	3
GT.USPT.	10748
GTS.USPT.	304
(POLY-A SAME GT).USPT.	11
("POLY-A" SAME "GT").USPT.	11

Display Format: TI | Change Format

Previous Page Next Page

WEST

Generate Collection | Print

Search Results - Record(s) 11 through 11 of 11 returned.

☐ 11. Document ID: US 5646247 A

L1: Entry 11 of 11 File: USPT Jul 8, 1997

US-PAT-NO: 5646247
DOCUMENT-IDENTIFIER: US 5646247 A

TITLE: Merozoite antigens localized at the apical end of the parasite

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

Generate Collection | Print

Term	Documents
POLY-A.USPT.	1384
POLY-AS.USPT.	3
GT.USPT.	10748
GTS.USPT.	304
(POLY-A SAME GT).USPT.	11
("POLY-A" SAME "GT").USPT.	11

Display Format: TI | Change Format

Previous Page Next Page

WEST

Generate Collection Print

L1: Entry 10 of 11 File: USPT Jan 13, 1998

DOCUMENT-IDENTIFIER: US 5707853 A
TITLE: Nucleic acid encoding calf intestinal alkaline phosphatase

Detailed Description Text (60):
The sequence and genomic structure of the b.IAP gene show high homology to all known TSAP genes. The smallest exon, exon VII, is only 73 bp long while the longest exon, exon XI, is approximately 1.1 kb long. The exact length of exon 11 cannot be determined since no cDNA with a poly-A tail had been isolated. The estimate given is based on the identification of a putative poly-adenylation site AATAAA (bp 5183-5188) in the 3' non-coding region of the gene (underlined in FIG. 1). The introns are among the smallest introns reported (Hawkins, Nucl. Acids Res. 16:9893-9908 (1988)) as was found in the case of other TSAP genes as well (Manes et al., supra; Hernthorn et al., supra; Knoll et al., supra; Millan and Manes, supra). The largest one, splitting exon V and exon VI, is only 257 bp long. All exon-intron junctions conform to the GT-AG rule (Breathnach et al., Proc. Natl. Acad. Sci. USA 75:4853-4857 (1978)) and also conform well to the consensus sequences (C/A) AG/GT(A/G)AGT (SEQ ID NO: 4) and (T/C).sub.n N(C/T)AG/G (SEQ ID NO: 5) for donor and acceptor sites, respectively (Mount, Nucl. Acids Res. 10:459-473 (1982)).

WEST

End of Result Set

Generate Collection Print

L6: Entry 20 of 20 File: USPT Jan 26, 1993

DOCUMENT-IDENTIFIER: US 5182205 A
TITLE: Nucleotide sequences which are selectively expressed in pre-B cells and probes therefor

Priority Application Year (1):
1986

Priority Application Year (2):
1987

Priority Application Year (3):
1987

Drawing Description Text (14):
FIG. 8 Nucleotide sequence of the 0.7 kb insert of clone pZ 183-1. The proposed poly(A) attachment site is underlined.

Drawing Description Text (22):
FIG. 14 Nucleotide sequence of the genomic form of .lambda.5 containing all cDNA sequences and the amino acid sequences deduced from them. cDNA sequences of the pZ183-1a clone are boxed. The sequences are divided into three parts which show the three exons and genomic sequences 5' and 3' adjacent to them. a and b indicate the major sites of initiation of transcription determined by the primer extension experiment shown in FIG. 17. The 18 nucleotides synthesized as a primer for the extension method are indicated with a broken line over the sequence. Sequences boxed in broken lines indicate the 5' part of exon I determined by this primer extension method (see FIG. 17). GT (donor) and AG (acceptor) splicing signal sequences of introns are underlined. The triplet indicated by three closed circles (.cndot.) above the sequence shows the possible translation start codon ATG. The sequence underlined by six circles shows the poly (A) addition signal sequence.

Drawing Description Text (27):
FIG. 17 Primer extension analysis of the 5' end of .lambda.5 mRNA. The synthetic oligonucleotide 5'-CAGAGTCTGTCCTACTCT-3' complementary to a 18 nucleotide sequence in Exon I (see FIG. 14, position 416-433) was labeled and hybridized to pre-B cell line 40E-1 poly A containing RNA (lane 1) and yeast t-RNA (lane 2).

Drawing Description Text (34):
FIG. 22 Nucleotide sequence and deduced amino acid sequence of the V.sub.preB 1 and V.sub.preB 2 gene. For V.sub.preB 1 nucleotide sequences of both the genomic form (7pB12-2) as well as of the cDNA (pZ121) are given. The cDNA sequences are identical with the genomic sequences and are, therefore, only indicated by dashes (--) and follows the genomic sequence in numbering. Numbering of amino acid residues starts with -19 as the first position of the leader and proceeds to +1 as the first position of the mature protein. The sequence marked by closed circles (.....) shows the poly A addition signal sequence. Arrows (.dwnarw.) indicate potential splice sites. The asterisk (*) points to the termination codon TAG. DNA sequencing was carried out using the dideoxy chain termination method by subcloning of fragments into M13mp18 and M13mp19 vectors, using a 17-mer universal M13 primer (Amersham). The V.sub.preB 2 nucleotide sequence of the genomic form (7pB70-1) is given. (For a restriction map of 7pB70-1, see FIG. 25). V.sub.preB 2 sequences identical to V.sub.preB 1 sequences are

indicated by dashes (--). Wherever the deduced amino acid sequence of V.sub.preB 2 differs from that of V.sub.preB 1 the changed am acid is given in brackets ( ).

Drawing Description Text (43):
FIG. 29 Northern blot analysis of poly(A)-selected RNA from lymphoid cells.

Drawing Description Text (44):
5 .mu.g poly(A).sup.+ RNA was applied to each lane, electrophoresed and blotted onto activated DPT paper. Identical filters were probed with: (A) a .sup.32 P-labelled 1.2 kb PstI fragment of pHVpB-6 or (B) a .sup.32 P-labelled 560 bp EcoRI-AccI fragment from pZ121. a mouse V.sub.preB 1 cDNA clone. The filter in panel (A) was washed finally in 0.2.times.SSC. 0.1% SDS at 65.degree. C., then exposed to x-ray film overnight at -80.degree. C. with intensifying screens. The filter in panel (B) was washed finally in 0.2.times.SSC, 0.1% SDS at 37.degree. C. and exposed as described above. Sizes of hybridizing bands were calculated using RNA molecular weight standards purchased from BRL (Bethesda, Md.).

Detailed Description Text (2):
The nucleotide sequences which are selectively expressed in pre-B cells may be identified by subtraction hybridization, i.e., by a method in which nucleotide sequences which are expressed in pre-B cells and in other cells are eliminated and only those sequences are selected which are solely expressed in pre-B cells. More specifically the nucleotide sequence is identified by preparing a cDNA library from poly A containing RNA from a pre-B cell and selecting from that library cDNA clones which hybridize to polysomal poly A containing RNA from a pre-B cell and not to polysomal poly A containing RNA from a different cell which is not a pre-B cell.

Detailed Description Text (4):
For identifying a first nucleotide sequence selectively expressed in pre-B cells mRNA, preferably microsome-bound polysomal poly A containing RNA can be isolated from pre-B cells by methods known in the art (e.g. Maniatis, et al., supra. pp. 188-209) or as described in the Example. Since it is difficult to isolate a sufficient number of such cells from a mammalian organism, especially from a human organism, a cell line derived from such a subset of the lymphoid cell population may be chosen.

Detailed Description Text (6):
A cDNA library, i.e., a collection of DNA's complementary to the poly A containing RNA from pre-B cells can be prepared by methods known in the art (e.g. Maniatis, et al., supra, pp. 211-246) or as described in the Example. Repeated subtraction hybridization using polysomal poly A containing RNA from a pre-B cell and from a cell which is not a pre-B cell is used to isolate a cDNA clone comprising a nucleotide sequence which is selectively expressed in pre-B cells. Suitable cells which are not pre-B cells are those distinctly different from cells of the early stages of the B cell lineage but related to the latter cells, so that they both express a similar subset of genes. Examples of such cells are lymphoid cells, e.g., T cells, preferably a T cell hybridoma.

Detailed Description Text (16):
In the present invention the selected 70Z/3 cDNA sequence hybridized specifically to a 1.2 kb size transcript present in a variety of pre-B cells. No hybridization was found under the same conditions using poly A containing RNA from mature B cells, plasma cells, T cells and other cells which are not from the B cell lineage. The selected 70Z/3 cDNA sequence is 380 nucleotide pairs long. It represents therefore only a partial cDNA of the 1.2 kb long transcript of the gene selectively expressed in pre-B cells.

Detailed Description Text (49):
Poly A containing RNA was prepared by repeated oligo(dT) cellulose chromatography (P-L Pharmacia, Uppsala, Sweden) in the presence of dimethyl sulfoxide as described by Bantle (Anal Biochem. 72, 413-427, [1976]).

Detailed Description Text (51):
A subtracted cDNA library for pre-B cell specific clones was constructed essentially according to the method of Davis et al. (supra). The first cDNA strand was synthesized with 10 .mu.g of microsome-bound polysomal poly A containing RNA from 70Z/3 in 50 mM

Tris-HCl, pH 8.3, 6 mM MgCl.sub.2, 60 mM NaCl, 20 mM dithiothreitol (DTT), 10 .mu.g/ml of oligo (dT.sub.12-18), 1 mM of each four deoxyribonucleotides 100 .mu.Ci of .sup.32 P-dCTP (.about.3000 Ci/mmol), 60 units/ml of placental ribonuclease inhibitor 100 .mu.g/ml of actinomycin D and 100 units of AMV reverse transcriptase (Stehlin, Co., Basle, Switzerland) at 40.degree. C. for 2 hours.

Detailed Description Text (52):
After RNA hydrolysis, hybridization reactions were performed in 0.5M phosphate buffer, 5 mM EDTA, 0.1% lithium laurylsulfate with twenty times excess amount of polysomal poly A containing RNA from a T cell hybridoma, e.g., from the T cell hybridoma K62 at 68.degree. C. for 16-20 hours to achieve a Cot of 2000. The single-stranded fraction after hydroxylapatite (Bio-Rad Laboratories, Richmond, CA, USA) chromatography in 0.12M phosphate buffer, 0.1% lithium laurylsulfate, 5 mM EDTA at 65.degree. C. was re-subtracted in the same conditions as above.

Detailed Description Text (57):
Prehybridization and hybridization were performed in 5.times.SSPE (750 mM NaCl, 50 mM NaH.sub.2 PO.sub.4, 5 mM EDTA; pH 7,4), 5.times.Denhardt's solution (Maniatis et al., supra, p. 327), 1% SDS, 1 .mu.g/ml tRNA from E. coli, 1 .mu.g/ml poly(A), 100 .mu.g/ml of denatured salmon sperm DNA at 68.degree. C. and the filters were washed finally with 0.1.times.SSC (1.times.SSC=standard saline citrate=150 mM NaCl, 15 mM trisodium citrate, pH 7,0), 1% SDS at 65.degree. C. The clones which showed positive after 7 days of exposure with intensifying screen at -70.degree. C. were rescreened with both probes. 200 individual phage clones were selected by this procedure out of 50,000 clones.

Detailed Description Text (59):
One radiolabeled insert DNA fragment designated pZ 183 was selected and used for hybridization with a panel of RNA preparations from various cells to show that the insert DNA fragment hybridizes selectively to poly A containing RNA from pre-B cells. Preferably, different cell lines of different lineages at different stages of differentiation are used. These cell lines are considered to be "frozen" at a certain stage of normal cell development and, thus, represent the phenotype of these normal counterparts.

Detailed Description Text (71):
The size of the pZ 183-specific transcript(s) was analyzed in RNA prepared from either unstimulated or LPS-stimulated 70Z/3 cells, by Northern blot analysis (FIG. 3). Cytoplasmic RNA was isolated (Chirgwin, et al., Biochemistry 18, 5294-5299, [1979]) from 70Z/3 cells cultured with or without LPS (10 .mu.g/ml) for 12 hours. The RNA was enriched for poly A containing RNA by oligo (dT) cellulose chromatography. One to forty micrograms of an RNA sample wee electrophoretically separated in an agarose/formaldehyde gel and transferred to nitrocellulose filters as described (Maniatis et al., supra, pp 382-389). Prehybridization and hybridization were performed as described in the sections of differential hybridization but with 50% formamide at 42.degree. C. The filters were finally washed with 0.2.times.SSC, 1% SDS at 65.degree. C.

Detailed Description Text (74):
RNA was prepared from cells of spleen, thymus, kidney bone marrow, lung, heart, brain and liver. Poly A containing RNA isolated from these organs (5 .mu.g each) and poly A containing RNA from 70Z/3 cells (2 .mu.g) were electrophoretically separated, stained with ethidium bromide (FIG. 4b). transferred to nitrocellulose filter and hybridized to radioactive pZ 183 probe (FIG. 4a). Blots were exposed to X-ray film for 7 days at -70.degree. C. in the presence of an intensifying screen. It is clear from the data presented in FIG. 4 that this analysis yielded no positive signals from RNA of all the organs tested. This indicated that the relative contribution of pre-B cells expressing pZ 183 in all of these organs must be too low in the total mixture of all other cells to be detectable by Northern gel analysis.

Detailed Description Text (80):
To obtain longer cDNA clones corresponding to the 1.2 kb transcript found in all pre-B cell lines, a new cDNA library was constructed. A poly A containing RNA preparation obtained from 70Z/3 cells by the tailing method (Maniatis, et al., supra, pp. 230-242) was inserted into the pUC-13 vector (Messing et al., supra). The new cDNA library was

screened with the 380 nucleotide pair long insert of the cDNA clone pZ 183. Nine cDNA clones were found positive in a total of 50 000 clones. The cDNA clone with the longest i.e., a 0.7 kb insert called pZ 183-1, was sequenced by the dideoxy chain termination method (Sanger, et al., supra). FIG. 7 shows the restriction enzyme sites used for generating the fragments which were used for cloning into M13 phage vector. The arrows indicate the length of the fragments generated and the direction in which the fragments were sequenced.

Detailed Description Text (81):
The nucleotide sequence of the cDNA clone pZ 183-1 is shown in FIG. 8. The 5' to 3' orientation was deduced from the location of the poly A tail and the poly A attachment site (underlined). Nucleotide positions are numbered from the most 5' position of the insert cDNA fragment.

Detailed Description Text (92):
From the above results it was clear that the clone pZ 183-1 did not correspond to the full-length 1.2 kb long transcript which is selectively expressed in pre-B cells. Therefore a cDNA library was constructed from poly A containing RNA of the uninduced murine pre-B lymphoma cell line 70Z/3 by the method described by Okayama et al. (Mol. Cell. Biol. 2, 161-170, [1982]). 5.times.10.sup.4 individual recombinant clones were screened with the radioactive insert of pZ 183-1 as described above.

Detailed Description Text (108):
The 5' end of mature .lambda..sub.5 mRNA in pre-B cells was determined by primer extension. A synthetic oligonucleotide 5'-CAGAGTCTGTCCTACTCT-3' complementary to a part of Exon I was labeled with .gamma.-.sup.32 P ATP using T4 polynucleotide kinase (Ingraham. et al., Mol. Cell. Biol. 6, 2923-2931, [1986]). Poly A containing RNA of the murine pre-B cell line 40E-1 was purified as described above. 500 ng of labeled oligonucleotides were annealed to either 10 .mu.g of 40E-1 poly A containing RNA or yeast transfer RNA in 50 mM Tris/HCl, pH 7.5, 75 mM KCl, 3 mM MgCl. Cloned Moloney murine leukemia virus reverse transcriptase (600 units) (Bethesda Research Laboratories) was added to each mixture and the reaction was carried out for 1 hour at 37.degree. C. in the presence of 0.5 mM dATP, dGTP, dCTP and dTTP, 10 mM dithiothreitol, 1 mg/ml BSA, 1000 U/ml of ribonuclease inhibitor (Stehelin, Basle) and 100 .mu.g/ml of actinomycin D.

Detailed Description Text (111):
A human fetal liver cDNA library in the vector .lambda.gt11 was obtained from Clontech Laboratories, Inc. (4055 Fabian Way, Palo Alto, Calif. 94303, USA--Catalog #HL 1005). 2.5.times.10.sup.6 recombinant phage clones were plated onto agar plates (Maniatis, et al., pp. 68-73) containing 25 .mu.g/ml ampicillin and were transferred to nitrocellulose filters as described (Benton. et al., supra). The filters were screened with a .sup.32 P-labelled 700 nucleotide pair fragment generated by cutting the plasmid pZ 183-1a with PvuII and HindIII (=mouse probe). Following digestion, the insert was separated by electrophoresis through a 1% low melting point agarose gel and radiolabeled with .sup.32 P-dATP by the Klenow fragment reaction with random hexanucleotide primers from calf thymus DNA (Feinberg, et al., supra). Prehybridization of the filters was done at 37.degree. C. in a solution containing 50% formamide, 5.times.SSPE, 0.1% SDS, 10.times. Denhardt's solution. 100 .mu.g/ml salmon sperm DNA, 1 .mu.g/ml E.coli RNA, and 1 .mu.g/ml poly(A). Hybridization of the filters was done in the same conditions with the addition of 1.times.10.sup.6 cpm/ml of .sup.32 P-labeled mouse probe.

Detailed Description Text (115):
In a library of 10.sup.6 once amplified cDNA clones constructed from 70Z/3 pre-B lymphoma poly A+ RNA around 100 positive clones were found. One out of seven strongly hybridizing clones found was selected because it appeared to have the longest insert. This clone, named pZ121 (FIG. 20), contains a 780 base pair long pre-B specific insert including 20 base pairs of poly A. The clone pZ121 was deposited on Apr. 23, 1987 at the Deutsche Sammlung von Mikroorganismen (DSM) in the form of a sample of E. coli DHI (pZ121), its accession number being DSM 4088.

Detailed Description Text (152):
One of the important characteristics of the mouse V.sub.pre-B 1 gene is its restricted expression in mouse pre-B cell lines and, therefore, the pattern of expression of

human V.sub.pre-B in human lymphoid lines by Northern blot analysis of poly(A)-selected RNA was examined.

Detailed Description Text (153):
Total RNA was isolated from cytoplasm after lysis of cells in 5% citric acid containing 0.1% NP-40 as described by Schibler et al. (J. Mol. Biol, 142, 93-116 [1980]) and further purified by oligo(dT) cellulose chromatography as described above. 5 .mu.g of poly(A) enriched RNA were electrophoresed through 1% agarose gels containing 18 mM Na.sub.2 HPO.sub.4, 2 mM NaH.sub.2 PO.sub.4 and 6% formaldehyde. Separated RNA was then blotted onto diazotized phenylthioether (DPT) paper (Schleicher and Schuell).

Detailed Description Text (154):
Prehybridization of filters was done at 45.degree. C. in solutions containing 5.times.SSPE (1.times.SSPE=150 mM NaCl, 10 mM NaH.sub.2 PO.sub.4, 1 mM EDTA), 5.times.Denhardt's, 2 mM glycine, 50% deionized formamide, 100 .mu.g/ml salmon sperm DNA, 20 .mu.g/ml yeast tRNA and 1 .mu.g/ml poly(A). Stringent hybridizations were done at 45.degree. C. in prehydridization solution lacking glycine but containing 10% dextran sulfate and 3.times.10.sup.6 cpm/ml .sup.32 P-labelled probe. Cross species hybridizations were done at 37.degree. C. in hybridization solution containing only 30% formamide. Stringent washes were done at 65.degree. C. in 0.2.times.SSC, 0.1% SDS. Cross species hybridization experiments were washed finally in 0.2.times.SSC, 0.1% SDS at 37.degree. C.

Detailed Description Text (155):
Human V.sub.preB is expressed only in pre-B cell lines 207, 697 (Findley et al., supra), Nalm-6 (Hurwitz et al., supra) but not in the cell lines LBW-4, Raji and Jurkat (FIG. 29). The human V.sub.preB poly(A).sup.+ mRNA is 0.85 kb in size, as is the mRNA of its mouse homologue, V.sub.preB 1. Under low stringency conditions the mouse V.sub.preB 1 gene also hybridizes to 0.85 kb RNA of human pre-B cell lines (FIG. 29). Similar intensities of hybridization and similar sizes of the RNAs which hybridize with the mouse V.sub.preB 1 probe and the human probe indicate that the same RNA molecules may hybridize to both probes. The upper band in FIG. 29B corresponds to the size of 28S ribosomal RNA and may be the result of crosshybridization of the mouse V.sub.preB 1 probe to human ribosomal RNA at low stringency. The pattern of RNA expression of human V.sub.preB, so far, follows that of V.sub.preB 1 and .lambda.5 in the mouse and indicates that human V.sub.preB is selectively expressed in human pre-B cell lines, but not in mature B cell or T cell lines.

WEST

Generate Collection | Print

Search Results - Record(s) 11 through 20 of 20 returned.

☐ 11. Document ID: US 5661003 A

L6: Entry 11 of 20 File: USPT Aug 26, 1997

US-PAT-NO: 5661003
DOCUMENT-IDENTIFIER: US 5661003 A

TITLE: Water channel

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 12. Document ID: US 5641668 A

L6: Entry 12 of 20 File: USPT Jun 24, 1997

US-PAT-NO: 5641668
DOCUMENT-IDENTIFIER: US 5641668 A

TITLE: Proteins having glycosyltransferase activity

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 13. Document ID: US 5629204 A

L6: Entry 13 of 20 File: USPT May 13, 1997

US-PAT-NO: 5629204
DOCUMENT-IDENTIFIER: US 5629204 A

TITLE: Peptide related to human programmed cell death and DNA encoding it

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 14. Document ID: US 5587359 A

L6: Entry 14 of 20 File: USPT Dec 24, 1996

US-PAT-NO: 5587359
DOCUMENT-IDENTIFIER: US 5587359 A

TITLE: Human derived glycoprotein, biologically active factor which includes

glycoprotein and pharmaceutical product

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 15. Document ID: US 5573933 A

L6: Entry 15 of 20 File: USPT Nov 12, 1996

US-PAT-NO: 5573933
DOCUMENT-IDENTIFIER: US 5573933 A

TITLE: Transgenic pigs

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 16. Document ID: US 5525508 A

L6: Entry 16 of 20 File: USPT Jun 11, 1996

US-PAT-NO: 5525508
DOCUMENT-IDENTIFIER: US 5525508 A

TITLE: Haemonchus contortus vaccine

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 17. Document ID: US 5362640 A

L6: Entry 17 of 20 File: USPT Nov 8, 1994

US-PAT-NO: 5362640
DOCUMENT-IDENTIFIER: US 5362640 A

TITLE: Ornithine carbamoyl transferase gene and utilization of the DNA

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 18. Document ID: US 5359036 A

L6: Entry 18 of 20 File: USPT Oct 25, 1994

US-PAT-NO: 5359036
DOCUMENT-IDENTIFIER: US 5359036 A

TITLE: Growth hormone-like glycoproteins

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

19. Document ID: US 5328836 A

L6: Entry 19 of 20 File: USPT Jul 12, 1994

US-PAT-NO: 5328836
DOCUMENT-IDENTIFIER: US 5328836 A

TITLE: Plasmids containing DNA encoding the amino acid sequence of TCF-II and use thereof

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

20. Document ID: US 5182205 A

L6: Entry 20 of 20 File: USPT Jan 26, 1993

US-PAT-NO: 5182205
DOCUMENT-IDENTIFIER: US 5182205 A

TITLE: Nucleotide sequences which are selectively expressed in pre-B cells and probes therefor

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

Generate Collection | Print

Term	Documents
@PRAY.USPT.	1107774
(5 AND (@PRAY <= "1999")).USPT.	20
(@PRAY <= 1999 AND (L5)).USPT.	20

Display Format: TI | Change Format

Previous Page Next Page

WEST

Generate Collection | Print

Search Results - Record(s) 1 through 10 of 20 returned.

1. Document ID: US 6472509 B1

L6: Entry 1 of 20 File: USPT Oct 29, 2002

US-PAT-NO: 6472509
DOCUMENT-IDENTIFIER: US 6472509 B1

TITLE: Feline cytokine protein

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

2. Document ID: US 6342376 B1

L6: Entry 2 of 20 File: USPT Jan 29, 2002

US-PAT-NO: 6342376
DOCUMENT-IDENTIFIER: US 6342376 B1

TITLE: Two-color differential display as a method for detecting regulated genes

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

3. Document ID: US 6333309 B1

L6: Entry 3 of 20 File: USPT Dec 25, 2001

US-PAT-NO: 6333309
DOCUMENT-IDENTIFIER: US 6333309 B1

TITLE: Human-derived glycoprotein, biologically active factor which includes glycoprotein, and pharmaceutical product which comprises biologically active factor as active component

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

4. Document ID: US 6193983 B1

L6: Entry 4 of 20 File: USPT Feb 27, 2001

US-PAT-NO: 6193983
DOCUMENT-IDENTIFIER: US 6193983 B1

TITLE: Equine herpesvirus glycoproteins

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 5. Document ID: US 6156516 A

L6: Entry 5 of 20 File: USPT Dec 5, 2000

US-PAT-NO: 6156516
DOCUMENT-IDENTIFIER: US 6156516 A

TITLE: Method for screening substance inhibiting activation of NF-.kappa.B

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 6. Document ID: US 5958721 A

L6: Entry 6 of 20 File: USPT Sep 28, 1999

US-PAT-NO: 5958721
DOCUMENT-IDENTIFIER: US 5958721 A

TITLE: Methods for screening of substances for therapeutic activity and yeast for use therein

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 7. Document ID: US 5942413 A

L6: Entry 7 of 20 File: USPT Aug 24, 1999

US-PAT-NO: 5942413
DOCUMENT-IDENTIFIER: US 5942413 A

TITLE: Nematode vaccine

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 8. Document ID: US 5922327 A

L6: Entry 8 of 20 File: USPT Jul 13, 1999

US-PAT-NO: 5922327
DOCUMENT-IDENTIFIER: US 5922327 A

TITLE: Equine herpes virus glycoproteins

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 9. Document ID: US 5785986 A

L6: Entry 9 of 20 File: USPT Jul 28, 1998

US-PAT-NO: 5785986
DOCUMENT-IDENTIFIER: US 5785986 A

TITLE: Water channel

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 10. Document ID: US 5698520 A

L6: Entry 10 of 20 File: USPT Dec 16, 1997

US-PAT-NO: 5698520
DOCUMENT-IDENTIFIER: US 5698520 A

TITLE: Peptide related to human programmed cell death and DNA encoding the same

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

Generate Collection | Print

Term	Documents
@PRAY.USPT.	1107774
(5 AND (@PRAY <= "1999")).USPT.	20
(@PRAY <= 1999 AND (L5)).USPT.	20

Display Format: TI Change Format

Previous Page Next Page

WEST

Generate Collection | Print

Search Results - Record(s) 1 through 10 of 33 returned.

1. Document ID: US 6462185 B1

L12: Entry 1 of 33 File: USPT Oct 8, 2002

US-PAT-NO: 6462185
DOCUMENT-IDENTIFIER: US 6462185 B1

TITLE: Floral organ-specific gene and its promoter sequence

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

2. Document ID: US 6413727 B1

L12: Entry 2 of 33 File: USPT Jul 2, 2002

US-PAT-NO: 6413727
DOCUMENT-IDENTIFIER: US 6413727 B1

TITLE: Diagnosis for mutant APC by immunoassay

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

3. Document ID: US 6365730 B1

L12: Entry 3 of 33 File: USPT Apr 2, 2002

US-PAT-NO: 6365730
DOCUMENT-IDENTIFIER: US 6365730 B1

TITLE: DNA-Armed ribozymes and minizymes

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

4. Document ID: US 6329141 B1

L12: Entry 4 of 33 File: USPT Dec 11, 2001

US-PAT-NO: 6329141
DOCUMENT-IDENTIFIER: US 6329141 B1

TITLE: Methods for transforming Phaffia strains, transformed Phaffia strains so

obtained and recombinant DNA in said methods

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 5. Document ID: US 6297041 B1

L12: Entry 5 of 33 File: USPT Oct 2, 2001

US-PAT-NO: 6297041
DOCUMENT-IDENTIFIER: US 6297041 B1

TITLE: MN gene and protein

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 6. Document ID: US 6238669 B1

L12: Entry 6 of 33 File: USPT May 29, 2001

US-PAT-NO: 6238669
DOCUMENT-IDENTIFIER: US 6238669 B1

TITLE: Proteins encoded by chicken anemia virus DNA and diagnostic kits and vaccines employing said proteins

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 7. Document ID: US 6204370 B1

L12: Entry 7 of 33 File: USPT Mar 20, 2001

US-PAT-NO: 6204370
DOCUMENT-IDENTIFIER: US 6204370 B1

TITLE: MN gene and protein

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 8. Document ID: US 6200788 B1

L12: Entry 8 of 33 File: USPT Mar 13, 2001

US-PAT-NO: 6200788
DOCUMENT-IDENTIFIER: US 6200788 B1

TITLE: .beta.-ketoacyl-ACP synthetase II enzymes and genes coding for same

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

9. Document ID: US 6136957 A

L12: Entry 9 of 33 File: USPT Oct 24, 2000

US-PAT-NO: 6136957
DOCUMENT-IDENTIFIER: US 6136957 A

TITLE: Antibodies which bind granulocyte-macrophane colony-stimulating factor receptor

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

10. Document ID: US 6118044 A

L12: Entry 10 of 33 File: USPT Sep 12, 2000

US-PAT-NO: 6118044
DOCUMENT-IDENTIFIER: US 6118044 A

TITLE: Transgenic animal allergy models and methods for their use

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

Generate Collection | Print

Term	Documents
SIGNAL.USPT.	833577
SIGNALS.USPT.	654885
SEQUENCE.USPT.	466647
SEQUENCES.USPT.	122745
POLY.USPT.	153988
POLIES.USPT.	6
POLYS.USPT.	105
A.USPT.	6579161
AS.USPT.	2402821
ADDITI$5	0
ADDITI.USPT.	16
(L8 AND (SIGNAL SAME SEQUENCE SAME ADDITI$5 SAME (POLY ADJ "A"))).USPT.	33

There are more results than shown above. Click here to view the entire set.

Display Format: TI Change Format

Previous Page Next Page

WEST

Generate Collection Print

L12: Entry 1 of 33 File: USPT Oct 8, 2002

DOCUMENT-IDENTIFIER: US 6462185 B1
TITLE: Floral organ-specific gene and its promoter sequence

Priority Application Year (1):
1996

Detailed Description Text (9):
The nucleotide sequence represented by SEQ ID NO:3 has the following characteristics among others. 1. It has 3 transcription initiation points at intervals of several nucleotides and these points are all A (adenine) following TC. Specifically, the transcription initiation points are the adenines (A) at positions 1122, 1125 and 1129. 2. There is a TATA box-like sequence (5'-TATATAA-3') (Corden et al. Science 209, 1406-1414, 1980) 30 bp upstream of the most upstream transcription initiation point. 3. There are 2 ATG sequences in the same reading frame, each being located 77 bp and 113 bp downstream of the most upstream transcription initiation point. 4. A termination codon (TGA) is located 21 bp upstream of the most upstream ATG (the first ATG). Moreover, there are two poly A signal-like sequences(5'-AATAAA-3') (Heidecker and Messing, Annu. Rev. Plant Physiol. 37, 439-466, 1986) in the terminator region. The term "terminator region" herein referrs to the region which is downstream of the termination codon.

Detailed Description Text (100):
The product obtained by using 75FW1 and 175RV1 had an intron of 85 bp having a 5'-GT-AG-3' sequence in the both ends thereof. Therefore, when the DNA of the genomic clone was employed as a template, a PCR product longer than that amplified by using cDNA as a template was amplified. This intron had a PstI site at the 3'-terminus.

Detailed Description Text (102):
The total genomic DNA of rice was digested with a restriction enzyme EcoRI and genomic Southern analysis was carried out by using the RPC175 gene as a probe. Thus a band with a weak signal appeared at about 1.6 kb in addition to the one with a strong signal at about 2.6 kb (FIG. 3). On the other hand, phage DNA was extracted from the above-mentioned 5 clones and digested with EcoRI followed by Southern hybridization with the use of RPC175 as a probe. As a result, it was found that the DNA fragments which formed hybridization with RPC175 were limited to those of 2.6 kb and 1.6 kb, which agreed with the results of the Southern analysis on the genomic DNA. It was known from the nucleotide sequence data, that RPC175 had the unique EcoRI site about 70 bp upstream of the 3'-terminus. Therefore, the 1.6 kb fragment with a weak signal was considered to have been detected due to the homology between the short region (about 70 bp) from the EcoRI to the poly A sites in the 3'-region of RPC175 cDNA employed as a probe and the genomic DNA fragment.

Detailed Description Text (115):
As a result, it was found that the whole nucleotide sequence of the RPG102 clone consisted of 2,636 bp and, when compared with the nucleotide sequence of the cDNA clone RPC175, two introns (85 bp and 199 bp) were contained in the region of the structural gene. The nucleotide sequences 5'GT and AG3' at both ends were conserved in both of these introns. The nucleotide sequences in the regions other than these introns of the genomic clone RPG102 coincided completely with the cDNA clone RPC175. A poly A signal-like sequence 5'-AATAAA-3' (Heidecker and Messing, Annu. Rev. PlantPhysiol. 37, 439-466, 1986) was located about 90 bp upstream of the EcoRI site in the 3' side and about 40 bp downstream of the translation termination codon TAG.

WEST

Generate Collection | Print

Search Results - Record(s) 11 through 20 of 33 returned.

☐ 11. Document ID: US 6117665 A

L12: Entry 11 of 33 File: USPT Sep 12, 2000

US-PAT-NO: 6117665
DOCUMENT-IDENTIFIER: US 6117665 A

TITLE: DNA molecules coding for debranching enzymes derived from plants

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

☐ 12. Document ID: US 6114124 A

L12: Entry 12 of 33 File: USPT Sep 5, 2000

US-PAT-NO: 6114124
DOCUMENT-IDENTIFIER: US 6114124 A

TITLE: Detection of APC proteins

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

☐ 13. Document ID: US 6093548 A

L12: Entry 13 of 33 File: USPT Jul 25, 2000

US-PAT-NO: 6093548
DOCUMENT-IDENTIFIER: US 6093548 A

TITLE: Detection and quantitation of MN-specific antibodies.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

☐ 14. Document ID: US 6083744 A

L12: Entry 14 of 33 File: USPT Jul 4, 2000

US-PAT-NO: 6083744
DOCUMENT-IDENTIFIER: US 6083744 A

TITLE: DNA-armed ribozymes and minizymes

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

☐ 15. Document ID: US 6077946 A

L12: Entry 15 of 33 File: USPT Jun 20, 2000

US-PAT-NO: 6077946
DOCUMENT-IDENTIFIER: US 6077946 A

TITLE: DNA encoding horseshoe crab amebocyte lysate factor G subunit A

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

☐ 16. Document ID: US 6069242 A

L12: Entry 16 of 33 File: USPT May 30, 2000

US-PAT-NO: 6069242
DOCUMENT-IDENTIFIER: US 6069242 A

TITLE: MN gene and protein

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

☐ 17. Document ID: US RE36713 E

L12: Entry 17 of 33 File: USPT May 23, 2000

US-PAT-NO: RE36713
DOCUMENT-IDENTIFIER: US RE36713 E

TITLE: APC gene and nucleic acid probes derived therefrom

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

☐ 18. Document ID: US 6051226 A

L12: Entry 18 of 33 File: USPT Apr 18, 2000

US-PAT-NO: 6051226
DOCUMENT-IDENTIFIER: US 6051226 A

TITLE: MN-specific antibodies and their use in cancer treatment

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

19. Document ID: US 6020201 A

L12: Entry 19 of 33 File: USPT Feb 1, 2000

US-PAT-NO: 6020201
DOCUMENT-IDENTIFIER: US 6020201 A

TITLE: Isolated nucleic acid molecules which encode mammalian or rodent 2,8 polysialyl transferases

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw. Desc

20. Document ID: US 5989838 A

L12: Entry 20 of 33 File: USPT Nov 23, 1999

US-PAT-NO: 5989838
DOCUMENT-IDENTIFIER: US 5989838 A

TITLE: Immunological methods of detecting MN proteins and MN polypeptides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw. Desc

Generate Collection | Print

Term	Documents
SIGNAL.USPT.	833577
SIGNALS.USPT.	654885
SEQUENCE.USPT.	466647
SEQUENCES.USPT.	122745
POLY.USPT.	153988
POLIES.USPT.	6
POLYS.USPT.	105
A.USPT.	6579161
AS.USPT.	2402821
ADDITI$5	0
ADDITI.USPT.	16
(L8 AND (SIGNAL SAME SEQUENCE SAME ADDITI$5 SAME (POLY ADJ "A"))).USPT.	33

There are more results than shown above. Click here to view the entire set.

Display Format: TI Change Format

Previous Page Next Page

WEST

Generate Collection Print

L12: Entry 27 of 33 File: USPT Oct 26, 1999

DOCUMENT-IDENTIFIER: US 5972353 A
TITLE: MN proteins, polypeptides, fusion proteins and fusion polypeptides

Priority Application Year (1):
1992

Detailed Description Text (22):
Based upon results of the RACE analysis, the full-length MN cDNA sequence was seen to contain a single ORF starting at position 12, with an ATG codon that is in a good context (GCGCATGG) with the rule proposed for translation initiation [Kozak, J. Cell. Biol., 108: 229-241 (1989)]. [See below under Mapping of MN Gene Transcription Initiation Site for fine mapping of the 5' end of the MN gene.] The AT rich 3' untranslated region contains a polyadenylation signal (AATAAA) preceding the end of the cDNA by 10 bp. Surprisingly, the sequence from the original clone as well as from four additional clones obtained from the same cDNA library did not reveal any poly(A) tail. Moreover, as indicated above, just downstream of the poly(A) signal we found an ATTTA motif that is thought to contribute to mRNA instability (Shaw and Kamen, supra). This fact raised the possibility that the poly (A) tail is missing due to the specific degradation of the MN mRNA.

Detailed Description Text (33):
Table 1 below lists the splice donor and acceptor sequences that conform to consensus splice sequences including the AG-GT motif [Mount, "A catalogue of splice junction sequences," Nucleic Acids Res. 10: 459-472 (1982)].

Detailed Description Text (41):
An RNase protection assay, as described above, was also used to verify also the 3' end of the MN cDNA. That was important with respect to our previous finding that the cDNA contains a poly(A) signal but lacks a poly(A) tail, which could be lost during the proposed degradation of MN mRNA due to the presence of an instability motif in its 3' untranslated region. RNP analysis of MN mRNA with the fragment of the genomic clone XE3 covering the region of interest corroborated our data from MN cDNA sequencing, since the 3' end of the protected fragment corresponded to the last base of MN cDNA (position 10,752 of the genomic sequence). That site also meets the requirement for the presence of a second signal in the genomic sequence that is needed for transcription termination and polyadenylation [McLauchlan et al., Nucleic Acids Res., 13: 1347 (1985)]. Motif TGTGTTAGT (nt 10,759-10,767) corresponds well to both the consensus sequence and the position of that signal within 22 bp downstream from the polyA signal (nt 10,737-10,742).

Detailed Description Paragraph Table (9):

SEQUENCE LISTING - - - - (1) GENERAL INFORMATION: - - (iii) NUMBER OF SEQUENCES: 86 - - - - (2) INFORMATION FOR SEQ ID NO: 1: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1522 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: cDNA - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #1: - - ACAGTCAGCC GCATGGCTCC CCTGTGCCCC AGCCCCTGGC TCCCTCTGTT GA - #TCCCGGCC 60 - - CCTGCTCCAG GCCTCACTGT GCAACTGCTG CTGTCACTGC TGCTTCTGAT GC - #CTGTCCAT 120 - - CCCCAGAGGT TGCCCCGGAT GCAGGAGGAT TCCCCCTTGG GAGGAGGCTC TT - #CTGGGGAA 180 - - GATGACCCAC TGGGCGAGGA GGATCTGCCC AGTGAAGAGG ATTCACCCAG AG - #AGGAGGAT 240 - - CCACCCGGAG AGGAGGATCT ACCTGGAGAG GAGGATCTAC CTGGAGAGGA GG - #ATCTACCT 300 - - GAAGTTAAGC CTAAATCAGA AGAAGAGGGC TCCCTGAAGT

TAGAGGATCT AC - #CTACTGTT 360 - - GAGGCTCCTG GAGATCCTCA AGAACCCCAG AATAATGCCC
ACAGGGACAA AG - #AAGGGGAT 420 - - GACCAGAGTC ATTGGCGCTA TGGAGGCGAC CCGCCCTGGC
CCCGGGTGTC CC - #CAGCCTGC 480 - - GCGGGCCGCT TCCAGTCCCC GGTGGATATC CGCCCCCAGC
TCGCCGCCTT CT - #GCCCGGCC 540 - - CTGCGCCCCC TGGAACTCCT GGGCTTCCAG CTCCCGCCGC
TCCCAGAACT GC - #GCCTGCGC 600 - - AACAATGGCC ACAGTGTGCA ACTGACCCTG CCTCCTGGGC
TAGAGATGGC TC - #TGGGTCCC 660 - - GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT CTGCACTGGG
GGGCTGCAGG TC - #GTCCGGGC 720 - - TCGGAGCACA CTGTGGAAGG CCACCGTTTC CCTGCCGAGA
TCCACGTGGT TC - #ACCTCAGC 780 - - ACCGCCTTTG CCAGAGTTGA CGAGGCCTTG GGGCGCCCGG
GAGGCCTGGC CG - #TGTTGGCC 840 - - GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC AGTGCCTATG
AGCAGTTGCT GT - #CTCGCTTG 900 - - GAAGAAATCG CTGAGGAAGG CTCAGAGACT CAGGTCCCAG
GACTGGACAT AT - #CTGCACTC 960 - - CTGCCCTCTG ACTTCAGCCG CTACTTCCAA TATGAGGGGT
CTCTGACTAC AC - #CGCCCTGT 1020 - - GCCCAGGGTG TCATCTGGAC TGTGTTTAAC CAGACAGTGA
TGCTGAGTGC TA - #AGCAGCTC 1080 - - CACACCCTCT CTGACACCCT GTGGGGACCT GGTGACTCTC
GGCTACAGCT GA - #ACTTCCGA 1140 - - GCGACGCAGC CTTTGAATGG GCGAGTGATT GAGGCCTCCT
TCCCTGCTGG AG - #TGGACAGC 1200 - - AGTCCTCGGG CTGCTGAGCC AGTCCAGCTG AATTCCTGCC
TGGCTGCTGG TG - #ACATCCTA 1260 - - GCCCTGGTTT TTGGCCTCCT TTTTGCTGTC ACCAGCGTCG
CGTTCCTTGT GC - #AGATGAGA 1320 - - AGGCAGCACA GAAGGGGAAC CAAAGGGGGT GTGAGCTACC
GCCCAGCAGA GG - #TAGCCGAG 1380 - - ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA TGTGAGAAGC
CAGCCAGAGG CA - #TCTGAGGG 1440 - - GGAGCCGGTA ACTGTCCTGT CCTGCTCATT ATGCCACTTC
CTTTTAACTG CC - #AAGAAATT 1500 - - TTTTAAAATA AATATTTATA AT - # - # 1522 - - - - (2)
INFORMATION FOR SEQ ID NO: 2: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 459 amino
- #acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear - - (ii) MOLECULE
TYPE: protein (A) DESCRIPTION: First - # 37 amino acids represent signal pe - #ptide,
and remaining amino acids represent - #mature protein - - (xi) SEQUENCE DESCRIPTION:
SEQ ID NO: - #2: - - Met Ala Pro Leu Cys Pro Ser Pro - # Trp Leu Pro Leu Leu Ile Pro
Ala -35 - # -30 - # -25 - - Pro Ala Pro Gly Leu Thr Val Gln - # Leu Leu Leu Ser Leu
Leu Leu Leu -20 - # -15 - # -10 - - Met Pro Val His Pro Gln Arg Leu - # Pro Arg Met
Gln Glu Asp Ser Pro -5 - # 1 - # 5 - # 10 - - Leu Gly Gly Gly Ser Ser Gly Glu - # Asp
Asp Pro Leu Gly Glu Glu Asp 15 - # 20 - # 25 - - Leu Pro Ser Glu Glu Asp Ser Pro - #
Arg Glu Glu Asp Pro Pro Gly Glu 30 - # 35 - # 40 - - Glu Asp Leu Pro Gly Glu Glu Asp -
Leu Pro Gly Glu Glu Asp Leu Pro 45 - # 50 - # 55 - - Glu Val Lys Pro Lys Ser Glu Glu
- # Glu Gly Ser Leu Lys Leu Glu Asp 60 - # 65 - # 70 - # 75 - - Leu Pro Thr Val Glu
Ala Pro Gly - # Asp Pro Gln Glu Pro Gln Asn Asn - # 80 - # 85 - # 90 - - Ala His Arg
Asp Lys Glu Gly Asp - # Asp Gln Ser His Trp Arg Tyr Gly 95 - # 100 - # 105 - - Gly Asp
Pro Pro Trp Pro Arg Val - # Ser Pro Ala Cys Ala Gly Arg Phe 110 - # 115 - # 120 - -
Gln Ser Pro Val Asp Ile Arg Pro - # Gln Leu Ala Ala Phe Cys Pro Ala 125 - # 130 - #
135 - - Leu Arg Pro Leu Glu Leu Leu Gly - # Phe Gln Leu Pro Pro Leu Pro Glu 140 - #
145 - # 150 - # 155 - - Leu Arg Leu Arg Asn Asn Gly His - # Ser Val Gln Leu Thr Leu
Pro Pro - # 160 - # 165 - # 170 - - Gly Leu Glu Met Ala Leu Gly Pro - # Gly Arg Glu
Tyr Arg Ala Leu Gln 175 - # 180 - # 185 - - Leu His Leu His Trp Gly Ala Ala - # Gly
Arg Pro Gly Ser Glu His Thr 190 - # 195 - # 200 - - Val Glu Gly His Arg Phe Pro Ala -
Glu Ile His Val Val His Leu Ser 205 - # 210 - # 215 - - Thr Ala Phe Ala Arg Val Asp
Glu - # Ala Leu Gly Arg Pro Gly Gly Leu 220 - # 225 - # 230 - # 235 - - Ala Val Leu
Ala Ala Phe Leu Glu - # Glu Gly Pro Glu Glu Asn Ser Ala - # 240 - # 245 - # 250 - -
Tyr Glu Gln Leu Leu Ser Arg Leu - # Glu Glu Ile Ala Glu Glu Gly Ser 255 - # 260 - #
265 - - Glu Thr Gln Val Pro Gly Leu Asp - # Ile Ser Ala Leu Leu Pro Ser Asp 270 - #
275 - # 280 - - Phe Ser Arg Tyr Phe Gln Tyr Glu - # Gly Ser Leu Thr Thr Pro Pro Cys
285 - # 290 - # 295 - - Ala Gln Gly Val Ile Trp Thr Val - # Phe Asn Gln Thr Val Met
Leu Ser 300 - # 305 - # 310 - # 315 - - Ala Lys Gln Leu His Thr Leu Ser - # Asp Thr
Leu Trp Gly Pro Gly Asp - # 320 - # 325 - # 330 - - Ser Arg Leu Gln Leu Asn Phe Arg -
Ala Thr Gln Pro Leu Asn Gly Arg 335 - # 340 - # 345 - - Val Ile Glu Ala Ser Phe Pro
Ala - # Gly Val Asp Ser Ser Pro Arg Ala 350 - # 355 - # 360 - - Ala Glu Pro Val Gln
Leu Asn Ser - # Cys Leu Ala Ala Gly Asp Ile Leu 365 - # 370 - # 375 - - Ala Leu Val
Phe Gly Leu Leu Phe - # Ala Val Thr Ser Val Ala Phe Leu 380 - # 385 - # 390 - # 395 -
- Val Gln Met Arg Arg Gln His Arg - # Arg Gly Thr Lys Gly Gly Val Ser - # 400 - # 405
- # 410 - - Tyr Arg Pro Ala Glu Val Ala Glu - # Thr Gly Ala 415 - # 420 - - - - (2)
INFORMATION FOR SEQ ID NO: 3: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base -
#pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii)
MOLECULE TYPE: DNA (genomic) - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: YES - -
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #3: - - CGCCCAGTGG GTCATCTTCC CCAGAAGAG - # -
29 - - - - (2) INFORMATION FOR SEQ ID NO: 4: - - (i) SEQUENCE CHARACTERISTICS: (A)
LENGTH: 19 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY:
linear - - (ii) MOLECULE TYPE: DNA (genomic) - - (iii) HYPOTHETICAL: NO - - (iv)
ANTI-SENSE: YES - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #4: - - GGAATCCTCC
TGCATCCGG - # - # - # 19 - - - - (2) INFORMATION FOR SEQ ID NO: 5: - - (i) SEQUENCE

CHARACTERISTICS: (A) LENGTH: 10898 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #5: - - GGATCCTGTT GACTCGTGAC CTTACCCCCA ACCCTGTGCT CTCTGAAACA TG - #AGCTGTGT 60
- - CCACTCAGGG TTAAATGGAT TAAGGGCGGT GCAAGATGTG CTTTGTTAAA CA - #GATGCTTG 120 - -
AAGGCAGCAT GCTCGTTAAG AGTCATCACC AATCCCTAAT CTCAAGTAAT CA - #GGGACACA 180 - -
AACACTGCGG AAGGCCGCAG GGTCCTCTGC CTAGGAAAAC CAGAGACCTT TG - #TTCACTTG 240 - -
TTTATCTGAC CTTCCCTCCA CTATTGTCCA TGACCCTGCC AAATCCCCCT CT - #GTGAGAAA 300 - -
CACCCAAGAA TTATCAATAA AAAAATAAAT TTAAAAAAAA AATACAAAAA AA - #AAAAAAAA 360 - -
AAAAAAAAAA GACTTACGAA TAGTTATTGA TAAATGAATA GCTATTGGTA AA - #GCCAAGTA 420 - -
AATGATCATA TTCAAAACCA GACGGCCATC ATCACAGCTC AAGTCTACCT GA - #TTTGATCT 480 - -
CTTTATCATT GTCATTCTTT GGATTCACTA GATTAGTCAT CATCCTCAAA AT - #TCTCCCCC 540 - -
AAGTTCTAAT TACGTTCCAA ACATTTAGGG GTTACATGAA GCTTGAACCT AC - #TACCTTCT 600 - -
TTGCTTTTGA GCCATGAGTT GTAGGAATGA TGAGTTTACA CCTTACATGC TG - #GGGATTAA 660 - -
TTTAAACTTT ACCTCTAAGT CAGTTGGGTA GCCTTTGGCT TATTTTTGTA GC - #TAATTTTG 720 - -
TAGTTAATGG ATGCACTGTG AATCTTGCTA TGATAGTTTT CCTCCACACT TT - #GCCACTAG 780 - -
GGGTAGGTAG GTACTCAGTT TTCAGTAATT GCTTACCTAA GACCCTAAGC CC - #TATTTCTC 840 - -
TTGTACTGGC CTTTATCTGT AATATGGGCA TATTTAATAC AATATAATTT TT - #GGAGTTTT 900 - -
TTTGTTTGTT TGTTTGTTTG TTTTTTTGAG ACGGAGTCTT GCATCTGTCA TG - #CCCAGGCT 960 - -
GGAGTAGCAG TGGTGCCATC TCGGCTCACT GCAAGCTCCA CCTCCCGAGT TC - #ACGCCATT 1020 - -
TTCCTGCCTC AGCCTCCCGA GTAGCTGGGA CTACAGGCGC CCGCCACCAT GC - #CCGGCTAA 1080 - -
TTTTTTGTAT TTTTGGTAGA GACGGGGTTT CACCGTGTTA GCCAGAATGG TC - #TCGATCTC 1140 - -
CTGACTTCGT GATCCACCCG CCTCGGCCTC CCAAAGTTCT GGGATTACAG GT - #GTGAGCCA 1200 - -
CCGCACCTGG CCAATTTTTT GAGTCTTTTA AAGTAAAAAT ATGTCTTGTA AG - #CTGGTAAC 1260 - -
TATGGTACAT TTCCTTTTAT TAATGTGGTG CTGACGGTCA TATAGGTTCT TT -

Detailed Description Paragraph Table (10):

#TGAGTTTG 1320 - - GCATGCATAT GCTACTTTTT GCAGTCCTTT CATTACATTT TTCTCTCTTC AT -
#TTGAAGAG 1380 - - CATGTTATAT CTTTTAGCTT CACTTGGCTT AAAAGGTTCT CTCATTAGCC TA -
#ACACAGTG 1440 - - TCATTGTTGG TACCACTTGG ATCATAAGTG GAAAAACAGT CAAGAAATTG CA -
#CAGTAATA 1500 - - CTTGTTTGTA AGAGGGATGA TTCAGGTGAA TCTGACACTA AGAAACTCCC CT -
#ACCTGAGG 1560 - - TCTGAGATTC CTCTGACATT GCTGTATATA GGCTTTTCCT TTGACAGCCT GT -
#GACTGCGG 1620 - - ACTATTTTTC TTAAGCAAGA TATGCTAAAG TTTTGTGAGC CTTTTTCCAG AG -
#AGAGGTCT 1680 - - CATATCTGCA TCAAGTGAGA ACATATAATG TCTGCATGTT TCCATATTTC AG -
#GAATGTTT 1740 - - GCTTGTGTTT TATGCTTTTA TATAGACAGG GAAACTTGTT CCTCAGTGAC CC -
#AAAAGAGG 1800 - - TGGGAATTGT TATTGGATAT CATCATTGGC CCACGCTTTC TGACCTTGGA AA -
#CAATTAAG 1860 - - GGTTCATAAT CTCAATTCTG TCAGAATTGG TACAAGAAAT AGCTGCTATG TT -
#TCTTGACA 1920 - - TTCCACTTGG TAGGAAATAA GAATGTGAAA CTCTTCAGTT GGTGTGTGTC CC -
#TNGTTTTT 1980 - - TTGCAATTTC CTTCTTACTG TGTTAAAAAA AAGTATGATC TTGCTCTGAG AG -
#GTGAGGCA 2040 - - TTCTTAATCA TGATCTTTAA AGATCAATAA TATAATCCTT TCAAGGATTA TG -
#TCTTTATT 2100 - - ATAATAAAGA TAATTTGTCT TTAACAGAAT CAATAATATA ATCCCTTAAA GG -
#ATTATATC 2160 - - TTTGCTGGGC GCAGTGGCTC ACACCTGTAA TCCCAGCACT TTGGGTGGCC AA -
#GGTGGAAG 2220 - - GATCAAATTT GCCTACTTCT ATATTATCTT CTAAAGCAGA ATTCATCTCT CT -
#TCCCTCAA 2280 - - TATGATGATA TTGACAGGGT TTGCCCTCAC TCACTAGATT GTGAGCTCCT GC -
#TCAGGGCA 2340 - - GGTAGCGTTT TTTGTTTTTG TTTTTGTTTT TCTTTTTTGA GACAGGGTCT TG -
#CTCTGTCA 2400 - - CCCAGGCCAG AGTGCAATGG TACAGTCTCA GCTCACTGCA GCCTCAACCG CC -
#TCGGCTCA 2460 - - AACCATCATC CCATTTCAGC CTCCTGAGTA GCTGGGACTA CAGGCACATG CC -
#ATTACACC 2520 - - TGGCTAATTT TTTTGTATTT CTAGTAGAGA CAGGGTTTGG CCATGTTGCC CG -
#GGCTGGTC 2580 - - TCGAACTCCT GGACTCAAGC AATCCACCCA CCTCAGCCTC CCAAAATGAG GG -
#ACCGTGTC 2640 - - TTATTCATTT CCATGTCCCT AGTCCATAGC CCAGTGCTGG ACCTATGGTA GT -
#ACTAAATA 2700 - - AATATTTGTT GAATGCAATA GTAAATAGCA TTTCAGGGAG CAAGAACTAG AT -
#TAACAAAG 2760 - - GTGGTAAAAG GTTTGGAGAA AAAAATAATA GTTTAATTTG GCTAGAGTAT GA -
#GGGAGAGT 2820 - - AGTAGGAGAC AAGATGGAAA GGTCTCTTGG GCAAGGTTTT GAAGGAAGTT GG -
#AAGTCAGA 2880 - - AGTACACAAT GTGCATATCG TGGCAGGCAG TGGGGAGCCA ATGAAGGCTT TT -
#GAGCAGGA 2940 - - GAGTAATGTG TTGAAAAATA AATATAGGTT AAACCTATCA GAGCCCCTCT GA -
#CACATACA 3000 - - CTTGCTTTTC ATTCAAGCTC AAGTTTGTCT CCCACATACC CATTACTTAA CT -
#CACCCTCG 3060 - - GGCTCCCCTA GCAGCCTGCC CTACCTCTTT ACCTGCTTCC TGGTGGAGTC AG -
#GGATGTAT 3120 - - ACATGAGCTG CTTTCCCTCT CAGCCAGAGG ACATGGGGGG CCCCAGCTCC CC -
#TGCCTTTC 3180 - - CCCTTCTGTG CCTGGAGCTG GGAAGCAGGC CAGGGTTAGC TGAGGCTGGC TG -
#GCAAGCAG 3240 - - CTGGGTGGTG CCAGGGAGAG CCTGCATAGT GCCAGGTGGT GCCTTGGGTT CC -
#AAGCTAGT 3300 - - CCATGGCCCC GATAACCTTC TGCCTGTGCA CACACCTGCC CCTCACTCCA CC -
#CCCATCCT 3360 - - AGCTTTGGTA TGGGGGAGAG GGCACAGGGC CAGACAAACC TGTGAGACTT TG -
#GCTCCATC 3420 - - TCTGCAAAAG GGCGCTCTGT GAGTCAGCCT GCTCCCCTCC AGGCTTGCTC CT -
#CCCCCACC 3480 - - CAGCTCTCGT TTCCAATGCA CGTACAGCCC GTACACACCG TGTGCTGGGA CA -
#CCCCACAG 3540 - - TCAGCCGCAT GGCTCCCCTG TGCCCCAGCC CCTGGCTCCC TCTGTTGATC CC -

```
#GGCCCCTG 3600 - - CTCCAGGCCT CACTGTGCAA CTGCTGCTGT CACTGCTGCT TCTGGTGCCT GT -
#CCATCCCC 3660 - - AGAGGTTGCC CCGGATGCAG GAGGATTCCC CCTTGGGAGG AGGCTCTTCT GG -
#GGAAGATG 3720 - - ACCCACTGGG CGAGGAGGAT CTGCCCAGTG AAGAGGATTC ACCCAGAGAG GA -
#GGATCCAC 3780 - - CCGGAGAGGA GGATCTACCT GGAGAGGAGG ATCTACCTGG AGAGGAGGAT CT -
#ACCTGAAG 3840 - - TTAAGCCTAA ATCAGAAGAA GAGGGCTCCC TGAAGTTAGA GGATCTACCT AC -
#TGTTGAGG 3900 - - CTCCTGGAGA TCCTCAAGAA CCCCAGAATA ATGCCCACAG GGACAAAGAA GG -
#TAAGTGGT 3960 - - CATCAATCTC CAAATCCAGG TTCCAGGAGG TTCATGACTC CCCTCCCATA CC -
#CCAGCCTA 4020 - - GGCTCTGTTC ACTCAGGGAA GGAGGGGAGA CTGTACTCCC CACAGAAGCC CT -
#TCCAGAGG 4080 - - TCCCATACCA ATATCCCCAT CCCCACTCTC GGAGGTAGAA AGGGACAGAT GT -
#GGAGAGAA 4140 - - AATAAAAAGG GTGCAAAAGG AGAGAGGTGA GCTGGATGAG ATGGGAGAGA AG -
#GGGGAGGC 4200 - - TGGAGAAGAG AAAGGGATGA GAACTGCAGA TGAGAGAAAA AATGTGCAGA CA -
#GAGGAAAA 4260 - - AAATAGGTGG AGAAGGAGAG TCAGAGAGTT TGAGGGGAAG AGAAAAGGAA AG -
#CTTGGGAG 4320 - - GTGAAGTGGG TACCAGAGAC AAGCAAGAAG AGCTGGTAGA AGTCATCTCA TC -
#TTAGGCTA 4380 - - CAATGAGGAA TTGAGACCTA GGAAGAAGGG ACACAGCAGG TAGAGAAACG TG -
#GCTTCTTG 4440 - - ACTCCCAAGC CAGGAATTTG GGGAAAGGGG TTGGAGACCA TACAAGGCAG AG -
#GGATGAGT 4500 - - GGGGAGAAGA AAGAAGGGAG AAAGGAAAGA TGGTGTACTC ACTCATTTGG GA -
#CTCAGGAC 4560 - - TGAAGTGCCC ACTCACTTTT TTTTTTTTTT TTTTTGAGAC AAACTTTCAC TT -
#TTGTTGCC 4620 - - CAGGCTGGAG TGCAATGGCG CGATCTCGGC TCACTGCAAC CTCCACCTCC CG -
#GGTTCAAG 4680 - - TGATTCTCCT GCCTCAGCCT CTAGCCAAGT AGCTGCGATT ACAGGCATGC GC -
#CACCACGC 4740 - - CCGGCTAATT TTTGTATTTT TAGTAGAGAC GGGGTTTCGC CATGTTGGTC AG -
#GCTGGTCT 4800 - - CGAACTCCTG ATCTCAGGTG ATCCAACCAC CCTGGCCTCC CAAAGTGCTG GG -
#ATTATAGG 4860 - - CGTGAGCCAC AGCGCCTGGC CTGAAGCAGC CACTCACTTT TACAGACCCT AA -
#GACAATGA 4920 - - TTGCAAGCTG GTAGGATTGC TGTTTGGCCC ACCCAGCTGC GGTGTTGAGT TT -
#GGGTGCGG 4980 - - TCTCCTGTGC TTTGCACCTG GCCCGCTTAA GGCATTTGTT ACCCGTAATG CT -
#CCTGTAAG 5040 - - GCATCTGCGT TTGTGACATC GTTTTGGTCG CCAGGAAGGG ATTGGGGCTC TA -
#AGCTTGAG 5100 - - CGGTTCATCC TTTTCATTTA TACAGGGGAT GACCAGAGTC ATTGGCGCTA TG -
#GAGGTGAG 5160 - - ACACCCACCC GCTGCACAGA CCCAATCTGG GAACCCAGCT CTGTGGATCT CC -
#CCTACAGC 5220 - - CGTCCCTGAA CACTGGTCCC GGGCGTCCCA CCCGCCGCCC ACCGTCCCAC CC -
#CCTCACCT 5280 - - TTTCTACCCG GGTTCCCTAA GTTCCTGACC TAGGCGTCAG ACTTCCTCAC TA -
#TACTCTCC 5340 - - CACCCCAGGC GACCCGCCCT GGCCCCGGGT GTCCCCAGCC TGCGCGGGCC GC -
#TTCCAGTC 5400 - - CCCGGTGGAT ATCCGCCCCC AGCTCGCCGC CTTCTGCCCG GCCCTGCGCC CC -
#CTGGAACT 5460 - - CCTGGGCTTC CAGCTCCCGC CGCTCCCAGA ACTGCGCCTG CGCAACAATG GC -
#CACAGTGG 5520 - - TGAGGGGGTC TCCCCGCCGA GACTTGGGGA TGGGGCGGGG CGCAGGGAAG GG -
#AACCGTCG 5580 - - CGCAGTGCCT GCCCGGGGGT TGGGCTGGCC CTACCGGGCG GGGCCGGCTC AC -
#TTGCCTCT 5640 - - CCCTACGCAG TGCAACTGAC CCTGCCTCCT GGGCTAGAGA TGGCTCTGGG TC -
#CCGGGCGG 5700 - - GAGTACCGGG CTCTGCAGCT GCATCTGCAC TGGGGGGCTG CAGGTCGTCC GG -
#GCTCGGAG 5760 - - CACACTGTGG AAGGCCACCG TTTCCCTGCC GAGGTGAGCG CGGACTGGCC GA -
#GAAGGGGC 5820 - - AAAGGAGCGG GGCGGACGGG GGCCAGAGAC GTGGCCCTCT CCTACCCTCG TG -
#TCCTTTTC 5880 - - AGATCCACGT GGTTCACCTC AGCACCGCCT TTGCCAGAGT TGACGAGGCC TT -
#GGGGCGCC 5940 - - CGGGAGGCCT GGCCGTGTTG GCCGCCTTTC TGGAGGTACC AGATCCTGGA CA -
#CCCCCTAC 6000 - - TCCCCGCTTT CCCATCCCAT GCTCCTCCCG GACTCTATCG TGGAGCCAGA GA -
#CCCCATCC 6060 - - CAGCAAGCTC ACTCAGGCCC CTGGCTGACA AACTCATTCA CGCACTGTTT GT -
#TCATTTAA 6120 - - CACCCACTGT GAACCAGGCA CCAGCCCCCA ACAAGGATTC TGAAGCTGTA GG -
#TCCTTGCC 6180 - - TCTAAGGAGC CCACAGCCAG TGGGGGAGGC TGACATGACA GACACATAGG AA -
#GGACATAG 6240 - - TAAAGATGGT GGTCACAGAG GAGGTGACAC TTAAAGCCTT CACTGGTAGA AA -
#AGAAAAGG 6300 - - AGGTGTTCAT TGCAGAGGAA ACAGAATGTG CAAAGACTCA GAATATGGCC TA -
#TTTAGGGA 6360 - - ATGGCTACAT ACACCATGAT TAGAGGAGGC CCAGTAAAGG GAAGGGATGG TG -
#AGATGCCT 6420 - - GCTAGGTTCA CTCACTCACT TTTATTTATT TATTTATTTT TTTGACAGTC TC -
#TCTGTCGC 6480 - - CCAGGCTGGA GTGCAGTGGT GTGATCTTGG GTCACTGCAA CTTCCGCCTC CC -
#GGGTTCAA 6540 - - GGGATTCTCC TGCCTCAGCT TCCTGAGTAG CTGGGGTTAC AGGTGTGTGC CA -
#CCATGCCC 6600 - - AGCTAATTTT TTTTTGTATT TTTAGTAGAC AGGGTTTCAC CATGTTGGTC AG -
#GCTGGTCT 6660 - - CAAACTCCTG GCCTCAAGTG ATCCGCCTGA CTCAGCCTAC CAAAGTGCTG AT -
#TACAAGTG 6720 - - TGAGCCACCG TGCCCAGCCA CACTCACTGA TTCTTTAATG CCAGCCACAC AG -
#CACAAAGT 6780 - - TCAGAGAAAT GCCTCCATCA TAGCATGTCA ATATGTTCAT ACTCTTAGGT TC -
#ATGATGTT 6840 - - CTTAACATTA GGTTCATAAG CAAAATAAGA AAAAAGAATA ATAAATAAAA GA -
#AGTGGCAT 6900 - - GTCAGGACCT CACCTGAAAA GCCAAACACA GAATCATGAA GGTGAATGCA GA -
#GGTGACAC 6960 - - CAACACAAAG GTGTATATAT GGTTTCCTGT GGGGAGTATG TACGGAGGCA GC -
#AGTGAGTG 7020 - - AGACTGCAAA CGTCAGAAGG GCACGGGTCA CTGAGAGCCT AGTATCCTAG TA -
#AAGTGGGC 7080 - - TCTCTCCCTC TCTCTCCAGC TTGTCATTGA AAACCAGTCC ACCAAGCTTG TT -
#GGTTCGCA 7140 - - CAGCAAGAGT ACATAGAGTT TGAAATAATA CATAGGATTT TAAGAGGGAG AC -
#ACTGTCTC 7200 - - TAAAAAAAAA AACAACAGCA ACAACAAAAA GCAACAACCA TTACAATTTT AT -
#GTTCCCTC 7260 - - AGCATTCTCA GAGCTGAGGA ATGGGAGAGG ACTATGGGAA CCCCCTTCAT GT -
#TCCGGCCT 7320 - - TCAGCCATGG CCCTGGATAC ATGCACTCAT CTGTCTTACA ATGTCATTCC CC -
#CAGGAGGG 7380 - - CCCGGAAGAA AACAGTGCCT ATGAGCAGTT GCTGTCTCGC TTGGAAGAAA TC -
#GCTGAGGA 7440 - - AGGTCAGTTT GTTGGTCTGG CCACTAATCT CTGTGGCCTA GTTCATAAAG AA -
```

#TCACCCTT 7500 - - TGGAGCTTCA GGTCTGAGGC TGGAGATGGG CTCCCTCCAG TGCAGGAGGG AT -
#TGAAGCAT 7560 - - GAGCCAGCGC TCATCTTGAT AATAACCATG AAGCTGACAG ACACAGTTAC CC -
#GCAAACGG 7620 - - CTGCCTACAG ATTGAAAACC AAGCAAAAAC CGCCGGGCAC GGTGGCTCAC GC -
#CTGTAATC 7680 - - CCAGCACTTT GGGAGGCCAA GGCAGGTGGA TCACGAGGTC AAGAGATCAA GA -
#CCATCCTG 7740 - - GCCAACATGG TGAAACCCCA TCTCTACTAA AAATACGAAA AAATAGCCAG GC -
#GTGGTGGC 7800 - - GGGTGCCTGT AATCCCAGCT ACTCGGGAGG CTGAGGCAGG AGAATGGCAT GA -
#ACCCGGGA 7860 - - GGCAGAAGTT GCAGTGAGCC GAGATCGTGC CACTGCACTC CAGCCTGGGC AA -
#CAGAGCGA 7920 - - GACTCTTGTC TCAAAAAAAA AAAAAAAAAA GAAAACCAAG CAAAAACCAA AA -
#TGAGACAA 7980 - - AAAAAACAAG ACCAAAAAAT GGTGTTTGGA AATTGTCAAG GTCAAGTCTG GA -
#GAGCTAAA 8040 - - CTTTTTCTGA GAACTGTTTA TCTTTAATAA GCATCAAATA TTTTAACTTT GT -
#AAATACTT 8100 - - TTGTTGGAAA TCGTTCTCTT CTTAGTCACT CTTGGGTCAT TTTAAATCTC AC -
#TTACTCTA 8160 - - CTAGACCTTT TAGGTTTCTG CTAGACTAGG TAGAACTCTG CCTTTGCATT TC -
#TTGTGTCT 8220 - - GTTTTGTATA GTTATCAATA TTCATATTTA TTTACAAGTT ATTCAGATCA TT -
#TTTTCTTT 8280 - - TCTTTTTTTT TTTTTTTTTT TTTTTTACAT CTTTAGTAGA GACAGGGTTT CA -
#CCATATTG 8340 - - GCCAGGCTGC TCTCAAACTC CTGACCTTGT GATCCACCAG CCTCGGCCTC CC -
#AAAGTGCT 8400 - - GGGATTCATT TTTTCTTTTT AATTTGCTCT GGGCTTAAAC TTGTGGCCCA GC -
#ACTTTATG 8460 - - ATGGTACACA GAGTTAAGAG TGTAGACTCA GACGGTCTTT CTTCTTTCCT TC -
#TCTTCCTT 8520 - - CCTCCCTTCC CTCCCACCTT CCCTTCTCTC CTTCCTTTCT TTCTTCCTCT CT -

Detailed Description Paragraph Table (11):

#TGCTTCCT 8580 - - CAGGCCTCTT CCAGTTGCTC CAAAGCCCTG TACTTTTTTT TGAGTTAACG TC -
#TTATGGGA 8640 - - AGGGCCTGCA CTTAGTGAAG AAGTGGTCTC AGAGTTGAGT TACCTTGGCT TC -
#TGGGAGGT 8700 - - GAAACTGTAT CCCTATACCC TGAAGCTTTA AGGGGGTGCA ATGTAGATGA GA -
#CCCCAACA 8760 - - TAGATCCTCT TCACAGGCTC AGAGACTCAG GTCCCAGGAC TGGACATATC TG -
#CACTCCTG 8820 - - CCCTCTGACT TCAGCCGCTA CTTCCAATAT GAGGGGTCTC TGACTACACC GC -
#CCTGTGCC 8880 - - CAGGGTGTCA TCTGGACTGT GTTTAACCAG ACAGTGATGC TGAGTGCTAA GC -
#AGGTGGGC 8940 - - CTGGGGTGTG TGTGGACACA GTGGGTGCGG GGGAAAGAGG ATGTAAGATG AG -
#ATGAGAAA 9000 - - CAGGAGAAGA AAGAAATCAA GGCTGGGCTC TGTGGCTTAC GCCTATAATC CC -
#ACCACGTT 9060 - - GGGAGGCTGA GGTGGGAGAA TGGTTTGAGC CCAGGAGTTC AAGACAAGGC GG -
#GGCAACAT 9120 - - AGTGTGACCC CATCTCTACC AAAAAAACCC CAACAAAACC AAAAATAGCC GG -
#GCATGGTG 9180 - - GTATGCGGCC TAGTCCCAGC TACTCAAGGA GGCTGAGGTG GGAAGATCGC TT -
#GATTCCAG 9240 - - GAGTTTGAGA CTGCAGTGAG CTATGATCCC ACCACTGCCT ACCATCTTTA GG -
#ATACATTT 9300 - - ATTTATTTAT AAAAGAAATC AAGAGGCTGG ATGGGGAATA CAGGAGCTGG AG -
#GGTGGAGC 9360 - - CCTGAGGTGC TGGTTGTGAG CTGGCCTGGG ACCCTTGTTT CCTGTCATGC CA -
#TGAACCCA 9420 - - CCCACACTGT CCACTGACCT CCCTAGCTCC ACACCCTCTC TGACACCCTG TG -
#GGGACCTG 9480 - - GTGACTCTCG GCTACAGCTG AACTTCCGAG CGACGCAGCC TTTGAATGGG CG -
#AGTGATTG 9540 - - AGGCCTCCTT CCCTGCTGGA GTGGACAGCA GTCCTCGGGC TGCTGAGCCA GG -
#TACAGCTT 9600 - - TGTCTGGTTT CCCCCCAGCC AGTAGTCCCT TATCCTCCCA TGTGTGTGCC AG -
#TGTCTGTC 9660 - - ATTGGTGGTC ACAGCCCGCC TCTCACATCT CCTTTTTCTC TCCAGTCCAG CT -
#GAATTCCT 9720 - - GCCTGGCTGC TGGTGAGTCT GCCCCTCCTC TTGGTCCTGA TGCCAGGAGA CT -
#CCTCAGCA 9780 - - CCATTCAGCC CCAGGGCTGC TCAGGACCGC CTCTGCTCCC TCTCCTTTTC TG -
#CAGAACAG 9840 - - ACCCCAACCC CAATATTAGA GAGGCAGATC ATGGTGGGGA TTCCCCCATT GT -
#CCCCAGAG 9900 - - GCTAATTGAT TAGAATGAAG CTTGAGAAAT CTCCCAGCAT CCCTCTCGCA AA -
#AGAATCCC 9960 - - CCCCCCTTTT TTTAAAGATA GGGTCTCACT CTGTTTGCCC CAGGCTGGGG TG -
#TTGTGGCA 10020 - - CGATCATAGC TCACTGCAGC CTCGAACTCC TAGGCTCAGG CAATCCTTTC AC -
#CTTAGCTT 10080 - - CTCAAAGCAC TGGGACTGTA GGCATGAGCC ACTGTGCCTG GCCCCAAACG GC -
#CCTTTTAC 10140 - - TTGGCTTTTA GGAAGCAAAA ACGGTGCTTA TCTTACCCCT TCTCGTGTAT CC -
#ACCCTCAT 10200 - - CCCTTGGCTG GCCTCTTCTG GAGACTGAGG CACTATGGGG CTGCCTGAGA AC -
#TCGGGGCA 10260 - - GGGGTGGTGG AGTGCACTGA GGCAGGTGTT GAGGAACTCT GCAGACCCCT CT -
#TCCTTCCC 10320 - - AAAGCAGCCC TCTCTGCTCT CCATCGCAGG TGACATCCTA GCCCTGGTTT TT -
#GGCCTCCT 10380 - - TTTTGCTGTC ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GG -
#TATTACAC 10440 - - TGACCCTTTC TTCAGGCACA AGCTTCCCCC ACCCTTGTGG AGTCACTTCA TG -
#CAAAGCGC 10500 - - ATGCAAATGA GCTGCTCCTG GGCCAGTTTT CTGATTAGCC TTTCCTGTTG TG -
#TACACACA 10560 - - GAAGGGGAAC CAAAGGGGGT GTGAGCTACC GCCCAGCAGA GGTAGCCGAG AC -
#TGGAGCCT 10620 - - AGAGGCTGGA TCTTGGAGAA TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GG -
#AGCCGGTA 10680 - - ACTGTCCTGT CCTGCTCATT ATGCCACTTC CTTTTAACTG CCAAGAAATT TT -
#TTAAAATA 10740 - - AATATTTATA ATAAAATATG TGTTAGTCAC CTTTGTTCCC CAAATCAGAA GG -
#AGGTATTT 10800 - - GAATTTCCTA TTACTGTTAT TAGCACCAAT TTAGTGGTAA TGCATTTATT CT -
#ATTACAGT 10860 - - TCGGCCTCCT TCCACACATC ACTCCAATGT GTTGCTCC - # - # 10898 - - - -
(2) INFORMATION FOR SEQ ID NO: 6: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37
amino - #acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear - - (ii)
MOLECULE TYPE: peptide (A) DESCRIPTION: Signa - #l peptide - - (xi) SEQUENCE
DESCRIPTION: SEQ ID NO: - #6: - - Met Ala Pro Leu Cys Pro Ser Pro - # Trp Leu Pro Leu
Leu Ile Pro Ala 1 - # 5 - # 10 - # 15 - - Pro Ala Pro Gly Leu Thr Val Gln - # Leu Leu
Leu Ser Leu Leu Leu Leu 20 - # 25 - # 30 - - Met Pro Val His Pro 35 - - - - (2)

INFORMATION FOR SEQ ID NO: 7: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: / - #desc = "primer" - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: YES - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #7: - - TGGGGTTCTT GAGGATCTCC AGGAG - # - # 25 - - - - (2) INFORMATION FOR SEQ ID NO: 8: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: / - #desc = "primer" - - (iii) HYPOTHETICAL: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #8: - - CTCTAACTTC AGGGAGCCCT CTTCTT - # - # 26 - - - - (2) INFORMATION FOR SEQ ID NO: 9: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: / - #desc = "primer" - - (iii) HYPOTHETICAL: NO - - (ix) FEATURE: N stands for inosine - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #9: - - CUACUACUAC UAGGCCACGC GTCGACTAGT ACGGGNNGGG NNGGGNNG - # 48 - - - - (2) INFORMATION FOR SEQ ID NO: 10: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 6 amino - #acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: peptide - - (v) FRAGMENT TYPE: internal - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #10: - - Glu Glu Asp Leu Pro Ser 1 5 - - - - (2) INFORMATION FOR SEQ ID NO: 11: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 6 amino - #acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: peptide - - (v) FRAGMENT TYPE: internal - - (ix) FEATURE: (A) NAME/KEY: Peptide (B) LOCATION:55..60 - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #11: - - Gly Glu Asp Asp Pro Leu 1 5 - - - - (2) INFORMATION FOR SEQ ID NO: 12: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 amino - #acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: peptide - - (v) FRAGMENT TYPE: internal - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #12: - - Asn Asn Ala His Arg Asp Lys Glu - # Gly Asp Asp Gln Ser His Trp Arg 1 - # 5 - # 10 - # 15 - - Tyr Gly Gly Asp Pro 20 - - - - (2) INFORMATION FOR SEQ ID NO: 13: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino - #acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: peptide - - (v) FRAGMENT TYPE: internal - - (ix) FEATURE: (A) NAME/KEY: Peptide (B) LOCATION:36..51 - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #13: - - His Pro Gln Arg Leu Pro Arg Met Gln Glu As - #p Ser Pro Leu Gly Gly 1 5 - # 10 - # 15 - - - - (2) INFORMATION FOR SEQ ID NO: 14: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 amino - #acids (B) TYPE: amino acid (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: peptide - - (v) FRAGMENT TYPE: internal - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #14: - - Glu Glu Asp Ser Pro Arg Glu Glu - # Asp Pro Pro Gly Glu Glu Asp Leu 1 - # 5 - # 10 - # 15 - - Pro Gly Glu Glu Asp Leu Pro Gly 20 - - - - (2) INFORMATION FOR SEQ ID NO: 15: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino - #acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: peptide - - (v) FRAGMENT TYPE: internal - - (ix) FEATURE: (A) NAME/KEY: Peptide (B) LOCATION:279..291 - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #15: - - Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Ty - #r Glu Gln 1 5 - # 10 - - - - (2) INFORMATION FOR SEQ ID NO: 16: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino - #acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: peptide - - (v) FRAGMENT TYPE: internal - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #16: - - Met Arg Arg Gln His Arg Arg Gly Thr Lys Gl - #y Gly Val Ser Tyr Arg 1 5 - # 10 - # 15 - - - - (2) INFORMATION FOR SEQ ID NO: 17: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #17: - - GTCGCTAGCT CCATGGGTCA TATGCAGAGG TTGCCCCGGA TGCAG - # - #45 - - - - (2) INFORMATION FOR SEQ ID NO: 18: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #18: - - GAAGATCTCT TACTCGAGCA TTCTCCAAGA TCCAGCCTCT AGG - # - # 43 - - - - (2) INFORMATION FOR SEQ ID NO: 19:

Detailed Description Paragraph Table (13):
- - GCTCAGAGAC TCAGGTCCCA GGACTGGACA TATCTGCACT CCTGCCCTCT GA - #CTTCAGCC 60 - - GCTACTTCCA ATATGAGGGG TCTCTGACTA CACCGCCCTG TGCCCAGGGT GT - #CATCTGGA 120 - - CTGTGTTTAA CCAGACAGTG ATGCTGAGTG CTAAGCAG - # - # 158 - - - - (2) INFORMATION FOR SEQ ID NO: 35: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 8th - #MN exon - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #35: - - CTCCACACCC TCTCTGACAC CCTGTGGGGA CCTGGTGACT CTCGGCTACA GC - #TGAACTTC 60 - - CGAGCGACGC AGCCTTTGAA TGGGCGAGTG ATTGAGGCCT CCTTCCCTGC TG - #GAGTGGAC 120 - - AGCAGTCCTC

GGGCTGCTGA GCCAG - # - # 145 - - - - (2) INFORMATION FOR SEQ ID NO: 36: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 9th - #MN exon - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #36: - - TCCAGCTGAA TTCCTGCCTG GCTGCTG - # - # 27 - - - - (2) INFORMATION FOR SEQ ID NO: 37: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 82 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 10th - #MN exon - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #37: - - GTGACATCCT AGCCCTGGTT TTTGGCCTCC TTTTTGCTGT CACCAGCGTC GC - #GTTCCTTG 60 - - TGCAGATGAG AAGGCAGCAC AG - # - # 82 - - - - (2) INFORMATION FOR SEQ ID NO: 38: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 11th - #MN exon - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #38: - - AAGGGGAACC AAAGGGGGTG TGAGCTACCG CCCAGCAGAG GTAGCCGAGA CT - #GGAGCCTA 60 - - GAGGCTGGAT CTTGGAGAAT GTGAGAAGCC AGCCAGAGGC ATCTGAGGGG GA - #GCCGGTAA 120 - - CTGTCCTGTC CTGCTCATTA TGCCACTTCC TTTTAACTGC CAAGAAATTT TT - #TAAAATAA 180 - - ATATTTATAA T - # - # - # 191 - - - - (2) INFORMATION FOR SEQ ID NO: 39: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1174 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 1st - #MN intron - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #39: - - GTAAGTGGTC ATCAATCTCC AAATCCAGGT TCCAGGAGGT TCATGACTCC CC - #TCCCATAC 60 - - CCCAGCCTAG GCTCTGTTCA CTCAGGGAAG GAGGGGAGAC TGTACTCCCC AC - #AGAAGCCC 120 - - TTCCAGAGGT CCCATACCAA TATCCCCATC CCCACTCTCG GAGGTAGAAA GG - #GACAGATG 180 - - TGGAGAGAAA ATAAAAAGGG TGCAAAAGGA GAGAGGTGAG CTGGATGAGA TG - #GGAGAGAA 240 - - GGGGGAGGCT GGAGAAGAGA AAGGGATGAG AACTGCAGAT GAGAGAAAAA AT - #GTGCAGAC 300 - - AGAGGAAAAA AATAGGTGGA GAAGGAGAGT CAGAGAGTTT GAGGGGAAGA GA - #AAAGGAAA 360 - - GCTTGGGAGG TGAAGTGGGT ACCAGAGACA AGCAAGAAGA GCTGGTAGAA GT - #CATCTCAT 420 - - CTTAGGCTAC AATGAGGAAT TGAGACCTAG GAAGAAGGGA CACAGCAGGT AG - #AGAAACGT 480 - - GGCTTCTTGA CTCCCAAGCC AGGAATTTGG GGAAAGGGGT TGGAGACCAT AC - #AAGGCAGA 540 - - GGGATGAGTG GGGAGAAGAA AGAAGGGAGA AAGGAAAGAT GGTGTACTCA CT - #CATTTGGG 600 - - ACTCAGGACT GAAGTGCCCA CTCACTTTTT TTTTTTTTTT TTTTGAGACA AA - #CTTTCACT 660 - - TTTGTTGCCC AGGCTGGAGT GCAATGGCGC GATCTCGGCT CACTGCAACC TC - #CACCTCCC 720 - - GGGTTCAAGT GATTCTCCTG CCTCAGCCTC TAGCCAAGTA GCTGCGATTA CA - #GGCATGCG 780 - - CCACCACGCC CGGCTAATTT TTGTATTTTT AGTAGAGACG GGGTTTCGCC AT - #GTTGGTCA 840 - - GGCTGGTCTC GAACTCCTGA TCTCAGGTGA TCCAACCACC CTGGCCTCCC AA - #AGTGCTGG 900 - - GATTATAGGC GTGAGCCACA GCGCCTGGCC TGAAGCAGCC ACTCACTTTT AC - #AGACCCTA 960 - - AGACAATGAT TGCAAGCTGG TAGGATTGCT GTTTGGCCCA CCCAGCTGCG GT - #GTTGAGTT 1020 - - TGGGTGCGGT CTCCTGTGCT TTGCACCTGG CCCGCTTAAG GCATTTGTTA CC - #CGTAATGC 1080 - - TCCTGTAAGG CATCTGCGTT TGTGACATCG TTTTGGTCGC CAGGAAGGGA TT - #GGGGCTCT 1140 - - AAGCTTGAGC GGTTCATCCT TTTCATTTAT ACAG - # - # 1174 - - - - (2) INFORMATION FOR SEQ ID NO: 40: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 193 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 2nd - #MN intron - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #40: - - GTGAGACACC CACCCGCTGC ACAGACCCAA TCTGGGAACC CAGCTCTGTG GA - #TCTCCCCT 60 - - ACAGCCGTCC CTGAACACTG GTCCCGGGCG TCCCACCCGC CGCCCACCGT CC - #CACCCCCT 120 - - CACCTTTTCT ACCCGGGTTC CCTAAGTTCC TGACCTAGGC GTCAGACTTC CT - #CACTATAC 180 - - TCTCCCACCC CAG - # - # - # 193 - - - - (2) INFORMATION FOR SEQ ID NO: 41: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 131 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 3rd - #MN intron - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #41: - - GTGAGGGGGT CTCCCCGCCG AGACTTGGGG ATGGGGCGGG GCGCAGGGAA GG - #GAACCGTC 60 - - GCGCAGTGCC TGCCCGGGGG TTGGGCTGGC CCTACCGGGC GGGGCCGGCT CA - #CTTGCCTC 120 - - TCCCTACGCA G - # - # - # 131 - - - - (2) INFORMATION FOR SEQ ID NO: 42: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 89 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 4th MN - # intron - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #42: - - GTGAGCGCGG ACTGGCCGAG AAGGGGCAAA GGAGCGGGGC GGACGGGGGC CA - #GAGACGTG 60 - - GCCCTCTCCT ACCCTCGTGT CCTTTTCAG - # - # 89 - - - - (2) INFORMATION FOR SEQ ID NO: 43: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1400 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 5th - #MN intron - - (iii) HYPOTHETICAL: NO - - (iv)

ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #43: - - GTACCAGATC
CTGGACACCC CCTACTCCCC GCTTTCCCAT CCCATGCTCC TC - #CCGGACTC 60 - - TATCGTGGAG
CCAGAGACCC CATCCCAGCA AGCTCACTCA GGCCCCTGGC TG - #ACAAACTC 120 - - ATTCACGCAC
TGTTTGTTCA TTTAACACCC ACTGTGAACC AGGCACCAGC CC - #CCAACAAG 180 - - GATTCTGAAG
CTGTAGGTCC TTGCCTCTAA GGAGCCCACA GCCAGTGGGG GA - #GGCTGACA 240 - - TGACAGACAC
ATAGGAAGGA CATAGTAAAG ATGGTGGTCA CAGAGGAGGT GA - #CACTTAAA 300 - - GCCTTCACTG
GTAGAAAAGA AAAGGAGGTG TTCATTGCAG AGGAAACAGA AT - #GTGCAAAG 360 - - ACTCAGAATA
TGGCCTATTT AGGGAATGGC TACATACACC ATGATTAGAG GA - #GGCCCAGT 420 - - AAAGGGAAGG
GATGGTGAGA TGCCTGCTAG GTTCACTCAC TCACTTTTAT TT - #ATTTATTT 480 - - ATTTTTTTGA
CAGTCTCTCT GTCGCCCAGG CTGGAGTGCA GTGGTGTGAT CT - #TGGGTCAC 540 - - TGCAACTTCC
GCCTCCCGGG TTCAAGGGAT TCTCCTGCCT CAGCTTCCTG AG - #TAGCTGGG 600 - - GTTACAGGTG
TGTGCCACCA TGCCCAGCTA ATTTTTTTTT GTATTTTTAG TA - #GACAGGGT 660 - - TTCACCATGT
TGGTCAGGCT GGTCTCAAAC TCCTGGCCTC AAGTGATCCG CC - #TGACTCAG 720 - - CCTACCAAAG
TGCTGATTAC AAGTGTGAGC CACCGTGCCC AGCCACACTC AC - #TGATTCTT 780 - - TAATGCCAGC
CACACAGCAC AAAGTTCAGA GAAATGCCTC CATCATAGCA TG - #TCAATATG 840 - - TTCATACTCT
TAGGTTCATG ATGTTCTTAA CATTAGGTTC ATAAGCAAAA TA - #AGAAAAAA 900 - - GAATAATAAA
TAAAAGAAGT GGCATGTCAG GACCTCACCT GAAAAGCCAA AC - #ACAGAATC 960 - - ATGAAGGTGA
ATGCAGAGGT GACACCAACA CAAAGGTGTA TATATGGTTT CC - #TGTGGGGA 1020 - - GTATGTACGG
AGGCAGCAGT GAGTGAGACT GCAAACGTCA GAAGGGCACG GG - #TCACTGAG 1080 - - AGCCTAGTAT
CCTAGTAAAG TGGGCTCTCT CCCTCTCTCT CCAGCTTGTC AT - #TGAAAACC 1140 - - AGTCCACCAA
GCTTGTTGGT TCGCACAGCA AGAGTACATA GAGTTTGAAA TA - #ATACATAG 1200 - - GATTTTAAGA
GGGAGACACT GTCTCTAAAA AAAAAAACAA CAGCAACAAC AA - #AAAGCAAC 1260 - - AACCATTACA
ATTTTATGTT CCCTCAGCAT TCTCAGAGCT GAGGAATGGG AG - #AGGACTAT 1320 - - GGGAACCCCC
TTCATGTTCC GGCCTTCAGC CATGGCCCTG GATACATGCA CT - #CATCTGTC 1380 - - TTACAATGTC
ATTCCCCCAG - # - # 140 - #0 - - - - (2) INFORMATION FOR SEQ ID NO: 44: - - (i)
SEQUENCE CHARACTERISTICS: (A) LENGTH: 1334 base - #pairs (B) TYPE: nucleic acid (C)
STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A)
DESCRIPTION: 6th - #MN intron - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - -
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #44: - - GTCAGTTTGT TGGTCTGGCC ACTAATCTCT
GTGGCCTAGT TCATAAAGAA TC - #ACCCTTTG 60 - - GAGCTTCAGG TCTGAGGCTG GAGATGGGCT
CCCTCCAGTG CAGGAGGGAT TG - #AAGCATGA 120 - - GCCAGCGCTC ATCTTGATAA TAACCATGAA
GCTGACAGAC ACAGTTACCC GC - #AAACGGCT 180 - - GCCTACAGAT TGAAAACCAA GCAAAAACCG
CCGGGCACGG TGGCTCACGC CT - #GTAATCCC 240 - - AGCACTTTGG GAGGCCAAGG CAGGTGGATC
ACGAGGTCAA GAGATCAAGA CC -

Detailed Description Paragraph Table (14):
#ATCCTGGC 300 - - CAACATGGTG AAACCCCATC TCTACTAAAA ATACGAAAAA ATAGCCAGGC GT -
#GGTGGCGG 360 - - GTGCCTGTAA TCCCAGCTAC TCGGGAGGCT GAGGCAGGAG AATGGCATGA AC -
#CCGGGAGG 420 - - CAGAAGTTGC AGTGAGCCGA GATCGTGCCA CTGCACTCCA GCCTGGGCAA CA -
#GAGCGAGA 480 - - CTCTTGTCTC AAAAAAAAAA AAAAAAAAGA AAACCAAGCA AAAACCAAAA TG -
#AGACAAAA 540 - - AAAACAAGAC CAAAAAATGG TGTTTGGAAA TTGTCAAGGT CAAGTCTGGA GA -
#GCTAAACT 600 - - TTTTCTGAGA ACTGTTTATC TTTAATAAGC ATCAAATATT TTAACTTTGT AA -
#ATACTTTT 660 - - GTTGGAAATC GTTCTCTTCT TAGTCACTCT TGGGTCATTT TAAATCTCAC TT -
#ACTCTACT 720 - - AGACCTTTTA GGTTTCTGCT AGACTAGGTA GAACTCTGCC TTTGCATTTC TT -
#GTGTCTGT 780 - - TTTGTATAGT TATCAATATT CATATTTATT TACAAGTTAT TCAGATCATT TT -
#TTCTTTTC 840 - - TTTTTTTTTT TTTTTTTTTT TTTTACATCT TTAGTAGAGA CAGGGTTTCA CC -
#ATATTGGC 900 - - CAGGCTGCTC TCAAACTCCT GACCTTGTGA TCCACCAGCC TCGGCCTCCC AA -
#AGTGCTGG 960 - - GATTCATTTT TTCTTTTTAA TTTGCTCTGG GCTTAAACTT GTGGCCCAGC AC -
#TTTATGAT 1020 - - GGTACACAGA GTTAAGAGTG TAGACTCAGA CGGTCTTTCT TCTTTCCTTC TC -
#TTCCTTCC 1080 - - TCCCTTCCCT CCCACCTTCC CTTCTCTCCT TCCTTTCTTT CTTCCTCTCT TG -
#CTTCCTCA 1140 - - GGCCTCTTCC AGTTGCTCCA AAGCCCTGTA CTTTTTTTTG AGTTAACGTC TT -
#ATGGGAAG 1200 - - GGCCTGCACT TAGTGAAGAA GTGGTCTCAG AGTTGAGTTA CCTTGGCTTC TG -
#GGAGGTGA 1260 - - AACTGTATCC CTATACCCTG AAGCTTTAAG GGGGTGCAAT GTAGATGAGA CC -
#CCAACATA 1320 - - GATCCTCTTC ACAG - # - # - # 1334 - - - - (2) INFORMATION FOR SEQ ID
NO: 45: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 512 base - #pairs (B) TYPE:
nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA
(genomic) (A) DESCRIPTION: 7th - #MN intron - - (iii) HYPOTHETICAL: NO - - (iv)
ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #45: - - GTGGGCCTGG
GGTGTGTGTG GACACAGTGG GTGCGGGGGA AAGAGGATGT AA - #GATGAGAT 60 - - GAGAAACAGG
AGAAGAAAGA AATCAAGGCT GGGCTCTGTG GCTTACGCCT AT - #AATCCCAC 120 - - CACGTTGGGA
GGCTGAGGTG GGAGAATGGT TTGAGCCCAG GAGTTCAAGA CA - #AGGCGGGG 180 - - CAACATAGTG
TGACCCCATC TCTACCAAAA AAACCCCAAC AAAACCAAAA AT - #AGCCGGGC 240 - - ATGGTGGTAT
GCGGCCTAGT CCCAGCTACT CAAGGAGGCT GAGGTGGGAA GA - #TCGCTTGA 300 - - TTCCAGGAGT
TTGAGACTGC AGTGAGCTAT GATCCCACCA CTGCCTACCA TC - #TTTAGGAT 360 - - ACATTTATTT
ATTTATAAAA GAAATCAAGA GGCTGGATGG GGAATACAGG AG - #CTGGAGGG 420 - - TGGAGCCCTG

AGGTGCTGGT TGTGAGCTGG CCTGGGACCC TTGTTTCCTG TC - #ATGCCATG 480 - - AACCCACCCA
CACTGTCCAC TGACCTCCCT AG - # - # 512 - - - - (2) INFORMATION FOR SEQ ID NO: 46: - -
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 114 base - #pairs (B) TYPE: nucleic acid (C)
STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A)
DESCRIPTION: 8th - #MN intron - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - -
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #46: - - GTACAGCTTT GTCTGGTTTC CCCCCAGCCA
GTAGTCCCTT ATCCTCCCAT GT - #GTGTGCCA 60 - - GTGTCTGTCA TTGGTGGTCA CAGCCCGCCT
CTCACATCTC CTTTTTCTCT CC - #AG 114 - - - - (2) INFORMATION FOR SEQ ID NO: 47: - - (i)
SEQUENCE CHARACTERISTICS: (A) LENGTH: 617 base - #pairs (B) TYPE: nucleic acid (C)
STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A)
DESCRIPTION: 9th - #MN intron - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - -
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #47: - - GTGAGTCTGC CCCTCCTCTT GGTCCTGATG
CCAGGAGACT CCTCAGCACC AT - #TCAGCCCC 60 - - AGGGCTGCTC AGGACCGCCT CTGCTCCCTC
TCCTTTTCTG CAGAACAGAC CC - #CAACCCCA 120 - - ATATTAGAGA GGCAGATCAT GGTGGGGATT
CCCCCATTGT CCCCAGAGGC TA - #ATTGATTA 180 - - GAATGAAGCT TGAGAAATCT CCCAGCATCC
CTCTCGCAAA AGAATCCCCC CC - #CCTTTTTT 240 - - TAAAGATAGG GTCTCACTCT GTTTGCCCCA
GGCTGGGGTG TTGTGGCACG AT - #CATAGCTC 300 - - ACTGCAGCCT CGAACTCCTA GGCTCAGGCA
ATCCTTTCAC CTTAGCTTCT CA - #AAGCACTG 360 - - GGACTGTAGG CATGAGCCAC TGTGCCTGGC
CCCAAACGGC CCTTTTACTT GG - #CTTTTAGG 420 - - AAGCAAAAAC GGTGCTTATC TTACCCCTTC
TCGTGTATCC ACCCTCATCC CT - #TGGCTGGC 480 - - CTCTTCTGGA GACTGAGGCA CTATGGGGCT
GCCTGAGAAC TCGGGGCAGG GG - #TGGTGGAG 540 - - TGCACTGAGG CAGGTGTTGA GGAACTCTGC
AGACCCCTCT TCCTTCCCAA AG - #CAGCCCTC 600 - - TCTGCTCTCC ATCGCAG - # - # - # 617 - - -
- (2) INFORMATION FOR SEQ ID NO: 48: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 130
base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - -
(ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 10th - #MN intron - - (iii)
HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: -
#48: - - GTATTACACT GACCCTTTCT TCAGGCACAA GCTTCCCCCA CCCTTGTGGA GT - #CACTTCAT 60 - -
GCAAAGCGCA TGCAAATGAG CTGCTCCTGG GCCAGTTTTC TGATTAGCCT TT - #CCTGTTGT 120 - -
GTACACACAG - # - # - # 130 - - - - (2) INFORMATION FOR SEQ ID NO: 49: - - (i) SEQUENCE
CHARACTERISTICS: (A) LENGTH: 1401 base - #pairs (B) TYPE: nucleic acid (C)
STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A)
DESCRIPTION: Spans - # 3' part of 1st intron to beyond end of - #5th exon - - (iii)
HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: -
#49: - - CAAACTTTCA CTTTTGTTGC CCAGGCTGGA GTGCAATGGC GCGATCTCGG CT - #CACTGCAA 60 - -
CCTCCACCTC CCGGGTTCAA GTGATTCTCC TGCCTCAGCC TCTAGCCAAG TA - #GCTGCGAT 120 - -
TACAGGCATG CGCCACCACG CCCGGCTAAT TTTTGTATTT TTAGTAGAGA CG - #GGGTTTCG 180 - -
CCATGTTGGT CAGGCTGGTC TCGAACTCCT GATCTCAGGT GATCCAACCA CC - #CTGGCCTC 240 - -
CCAAAGTGCT GGGATTATAG GCGTGAGCCA CAGCGCCTGG CCTGAAGCAG CC - #ACTCACTT 300 - -
TTACAGACCC TAAGACAATG ATTGCAAGCT GGTAGGATTG CTGTTTGGCC CA - #CCCAGCTG 360 - -
CGGTGTTGAG TTTGGGTGCG GTCTCCTGTG CTTTGCACCT GGCCCGCTTA AG - #GCATTTGT 420 - -
TACCCGTAAT GCTCCTGTAA GGCATCTGCG TTTGTGACAT CGTTTTGGTC GC - #CAGGAAGG 480 - -
GATTGGGGCT CTAAGCTTGA GCGGTTCATC CTTTTCATTT ATACAGGGGA TG - #ACCAGAGT 540 - -
CATTGGCGCT ATGGAGGTGA GACACCCACC CGCTGCACAG ACCCAATCTG GG - #AACCCAGC 600 - -
TCTGTGGATC TCCCCTACAG CCGTCCCTGA ACACTGGTCC CGGGCGTCCC AC - #CCGCCGCC 660 - -
CACCGTCCCA CCCCCTCACC TTTTCTACCC GGGTTCCCTA AGTTCCTGAC CT - #AGGCGTCA 720 - -
GACTTCCTCA CTATACTCTC CCACCCCAGG CGACCCGCCC TGGCCCCGGG TG - #TCCCCAGC 780 - -
CTGCGCGGGC CGCTTCCAGT CCCCGGTGGA TATCCGCCCC CAGCTCGCCG CC - #TTCTGCCC 840 - -
GGCCCTGCGC CCCCTGGAAC TCCTGGGCTT CCAGCTCCCG CCGCTCCCAG AA - #CTGCGCCT 900 - -
GCGCAACAAT GGCCACAGTG GTGAGGGGGT CTCCCCGCCG AGACTTGGGG AT - #GGGGCGGG 960 - -
GCGCAGGGAA GGGAACCGTC GCGCAGTGCC TGCCCGGGGG TTGGGCTGGC CC - #TACCGGGC 1020 - -
GGGGCCGGCT CACTTGCCTC TCCCTACGCA GTGCAACTGA CCCTGCCTCC TG - #GGCTAGAG 1080 - -
ATGGCTCTGG GTCCCGGGCG GGAGTACCGG GCTCTGCAGC TGCATCTGCA CT - #GGGGGGCT 1140 - -
GCAGGTCGTC CGGGCTCGGA GCACACTGTG GAAGGCCACC GTTTCCCTGC CG - #AGGTGAGC 1200 - -
GCGGACTGGC CGAGAAGGGG CAAAGGAGCG GGGCGGACGG GGGCCAGAGA CG - #TGGCCCTC 1260 - -
TCCTACCCTC GTGTCCTTTT CAGATCCACG TGGTTCACCT CAGCACCGCC TT - #TGCCAGAG 1320 - -
TTGACGAGGC CTTGGGGCGC CCGGGAGGCC TGGCCGTGTT GGCCGCCTTT CT - #GGAGGTAC 1380 - -
CAGATCCTGG ACACCCCCTA C - # - # 1401 - - - - (2) INFORMATION FOR SEQ ID NO: 50: - -
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 98 amino - #acids (B) TYPE: amino acid (D)
TOPOLOGY: linear - - (ii) MOLECULE TYPE: protein (A) DESCRIPTION: Regio - #n of
homology to collagen alpha 1 chain - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #50: -
- Gln Arg Leu Pro Arg Met Gln Glu - # Asp Ser Pro Leu Gly Gly Gly Ser 1 - # 5 - # 10 -
15 - - Ser Gly Glu Asp Asp Pro Leu Gly - # Glu Glu Asp Leu Pro Ser Glu Glu 20 - # 25
- # 30 - - Asp Ser Pro Arg Glu Glu Asp Pro - # Pro Gly Glu Glu Asp Leu Pro Gly 35 - #
40 - # 45 - - Glu Glu Asp Leu Pro Gly Glu Glu - # Asp Leu Pro Glu Val Lys Pro Lys 50 -
55 - # 60 - - Ser Glu Glu Glu Gly Ser Leu Lys - # Leu Glu Asp Leu Pro Thr Val Glu 65

- # 70 - # 75 - # 80 - - Ala Pro Gly Asp Pro Gln Glu Pro - # Gln Asn Asn Ala His Arg Asp Lys - # 85 - # 90 - # 95 - - Glu Gly - - - - (2) INFORMATION FOR SEQ ID NO: 51: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 amino - #acids (B) TYPE: amino acid (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: protein (A) DESCRIPTION: carbo - #nic anhydrase domain - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #51: - - Asp Asp Gln Ser His Trp Arg Tyr - # Gly Gly Asp Pro Pro Trp Pro Arg 1 - # 5 - # 10 - # 15 - - Val Ser Pro Ala Cys Ala Gly Arg - # Phe Gln Ser Pro Val Asp Ile Arg 20 - # 25 - # 30 - - Pro Gln Leu Ala Ala Phe Cys Pro - # Ala Leu Arg Pro Leu Glu Leu Leu 35 - # 40 - # 45 - - Gly Phe Gln Leu Pro Pro Leu Pro - # Glu Leu Arg Leu Arg Asn Asn Gly 50 - # 55 - # 60

Detailed Description Paragraph Table (15):

- - His Ser Val Gln Leu Thr Leu Pro - # Pro Gly Leu Glu Met Ala Leu Gly 65 - # 70 - # 75 - # 80 - - Pro Gly Arg Glu Tyr Arg Ala Leu - # Gln Leu His Leu His Trp Gly Ala - # 85 - # 90 - # 95 - - Ala Gly Arg Pro Gly Ser Glu His - # Thr Val Glu Gly His Arg Phe Pro 100 - # 105 - # 110 - - Ala Glu Ile His Val Val His Leu - # Ser Thr Ala Phe Ala Arg Val Asp 115 - # 120 - # 125 - - Glu Ala Leu Gly Arg Pro Gly Gly - # Leu Ala Val Leu Ala Ala Phe Leu 130 - # 135 - # 140 - - Glu Glu Gly Pro Glu Glu Asn Ser - # Ala Tyr Glu Gln Leu Leu Ser Arg 145 - # 150 - # 155 - # 160 - - Leu Glu Glu Ile Ala Glu Glu Gly - # Ser Glu Thr Gln Val Pro Gly Leu - # 165 - # 170 - # 175 - - Asp Ile Ser Ala Leu Leu Pro Ser - # Asp Phe Ser Arg Tyr Phe Gln Tyr 180 - # 185 - # 190 - - Glu Gly Ser Leu Thr Thr Pro Pro - # Cys Ala Gln Gly Val Ile Trp Thr 195 - # 200 - # 205 - - Val Phe Asn Gln Thr Val Met Leu - # Ser Ala Lys Gln Leu His Thr Leu 210 - # 215 - # 220 - - Ser Asp Thr Leu Trp Gly Pro Gly - # Asp Ser Arg Leu Gln Leu Asn Phe 225 - # 230 - # 235 - # 240 - - Arg Ala Thr Gln Pro Leu Asn Gly - # Arg Val Ile Glu Ala Ser Phe Pro - # 245 - # 250 - # 255 - - - - (2) INFORMATION FOR SEQ ID NO: 52: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino - #acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: peptide (A) DESCRIPTION: trans - #membrane region - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #52: - - Asp Ile Leu Ala Leu Val Phe Gly - # Leu Leu Phe Ala Val Thr Ser Val 1 - # 5 - # 10 - # 15 - - Ala Phe Leu Val 20 - - - - (2) INFORMATION FOR SEQ ID NO: 53: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 amino - #acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: peptide (A) DESCRIPTION: intra - #cellular C-terminus - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #53: - - Met Arg Arg Gln His Arg Arg Gly - # Thr Lys Gly Gly Val Ser Tyr Arg 1 - # 5 - # 10 - # 15 - - Pro Ala Glu Val Ala Glu Thr Gly - # Ala 20 - # 25 - - - - (2) INFORMATION FOR SEQ ID NO: 54: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 170 amino - #acids (B) TYPE: amino acid (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: protein - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #54: - - Arg Ala Leu Gln Leu His Leu His - # Trp Gly Ala Ala Gly Arg Pro Gly 1 - # 5 - # 10 - # 15 - - Ser Glu His Thr Val Glu Gly His - # Arg Phe Pro Ala Glu Ile His Val 20 - # 25 - # 30 - - Val His Leu Ser Thr Ala Phe Ala - # Arg Val Asp Glu Ala Leu Gly Arg 35 - # 40 - # 45 - - Pro Gly Gly Leu Ala Val Leu Ala - # Ala Phe Leu Glu Glu Gly Pro Glu 50 - # 55 - # 60 - - Glu Asn Ser Ala Tyr Glu Gln Leu - # Leu Ser Arg Leu Glu Glu Ile Ala 65 - # 70 - # 75 - # 80 - - Glu Glu Gly Ser Glu Thr Gln Val - # Pro Gly Leu Asp Ile Ser Ala Leu - # 85 - # 90 - # 95 - - Leu Pro Ser Asp Phe Ser Arg Tyr - # Phe Gln Tyr Glu Gly Ser Leu Thr 100 - # 105 - # 110 - - Thr Pro Pro Cys Ala Gln Gly Val - # Ile Trp Thr Val Phe Asn Gln Thr 115 - # 120 - # 125 - - Val Met Leu Ser Ala Lys Gln Leu - # His Thr Leu Ser Asp Thr Leu Trp 130 - # 135 - # 140 - - Gly Pro Gly Asp Ser Arg Leu Gln - # Leu Asn Phe Arg Ala Thr Gln Pro 145 - # 150 - # 155 - # 160 - - Leu Asn Gly Arg Val Ile Glu Ala - # Ser Phe - # 165 - # 170 - - - - (2) INFORMATION FOR SEQ ID NO: 55: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 470 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: RNA - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #55: - - CAUGGCCCCG AUAACCUUCU GCCUGUGCAC ACACCUGCCC CUCACUCCAC CC - #CCAUCCUA 60 - - GCUUUGGUAU GGGGGAGAGG GCACAGGGCC AGACAAACCU GUGAGACUUU GG - #CUCCAUCU 120 - - CUGCAAAAGG GCGCUCUGUG AGUCAGCCUG CUCCCCUCCA GGCUUGCUCC UC - #CCCCACCC 180 - - AGCUCUCGUU UCCAAUGCAC GUACAGCCCG UACACACCGU GUGCUGGGAC AC - #CCCACAGU 240 - - CAGCCGCAUG GCUCCCCUGU GCCCCAGCCC CUGGCUCCCU CUGUUGAUCC CG - #GCCCCUGC 300 - - UCCAGGCCUC ACUGUGCAAC UGCUGCUGUC ACUGCUGCUU CUGGUGCCUG UC - #CAUCCCCA 360 - - GAGGUUGCCC CGGAUGCAGG AGGAUUCCCC CUUGGGAGGA GGCUCUUCUG GG - #GAAGAUGA 420 - - CCCACUGGGC GAGGAGGAUC UGCCCAGUGA AGAGGAUUCA CCCAGAGAGG - # 470 - - - - (2) INFORMATION FOR SEQ ID NO: 56: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: Alu - #repeat within MN genomic region - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #56: - - GTTTTTTTGA GACGGAGTCT TGCATCTGTC ATGCCCAGGC TGGAGTAGCA GT - #GGTGCCAT 60 - -

CTCGGCTCAC TGCAAGCTCC ACCTCCCGAG TTCACGCCAT TTTCCTGCCT CA - #GCCTCCCG 120 - -
AGTAGCTGGG ACTACAGGCG CCCGCCACCA TGCCCGGCTA ATTTTTTGTA TT - #TTTGGTAG 180 - -
AGACGGGGTT TCACCGTGTT AGCCAGAATG GTCTCGATCT CCTGACTTCG TG - #ATCCACCC 240 - -
GCCTCGGCCT CCCAAAGTTC TGGGATTACA GGTGTGAGCC ACCGCACCTG GC - # 292 - - - - (2)
INFORMATION FOR SEQ ID NO: 57: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 262 base
- #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii)
MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: Alu - #repeat within MN genomic region -
- (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID
NO: - #57: - - TTTCTTTTTT GAGACAGGGT CTTGCTCTGT CACCCAGGCC AGAGTGCAAT GG - #TACAGTCT
60 - - CAGCTCACTG CAGCCTCAAC CGCCTCGGCT CAAACCATCA TCCCATTTCA GC - #CTCCTGAG 120 - -
TAGCTGGGAC TACAGGCACA TGCCATTACA CCTGGCTAAT TTTTTTGTAT TT - #CTAGTAGA 180 - -
GACAGGGTTT GGCCATGTTG CCCGGGCTGG TCTCGAACTC CTGGACTCAA GC - #AATCCACC 240 - -
CACCTCAGCC TCCCAAAATG AG - # - # 262 - - - - (2) INFORMATION FOR SEQ ID NO: 58: - -
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 904 base - #pairs (B) TYPE: nucleic acid (C)
STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) - -
(iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID
NO: - #58: - - GCTGGTCTCG AACTCCTGGA CTCAAGCAAT CCACCCACCT CAGCCTCCCA AA - #ATGAGGGA
60 - - CCGTGTCTTA TTCATTTCCA TGTCCCTAGT CCATAGCCCA GTGCTGGACC TA - #TGGTAGTA 120 - -
CTAAATAAAT ATTTGTTGAA TGCAATAGTA AATAGCATTT CAGGGAGCAA GA - #ACTAGATT 180 - -
AACAAAGGTG GTAAAAGGTT TGGAGAAAAA AATAATAGTT TAATTTGGCT AG - #AGTATGAG 240 - -
GGAGAGTAGT AGGAGACAAG ATGGAAAGGT CTCTTGGGCA AGGTTTTGAA GG - #AAGTTGGA 300 - -
AGTCAGAAGT ACACAATGTG CATATCGTGG CAGGCAGTGG GGAGCCAATG AA - #GGCTTTTG 360 - -
AGCAGGAGAG TAATGTGTTG AAAAATAAAT ATAGGTTAAA CCTATCAGAG CC - #CCTCTGAC 420 - -
ACATACACTT GCTTTTCATT CAAGCTCAAG TTTGTCTCCC ACATACCCAT TA - #CTTAACTC 480 - -
ACCCTCGGGC TCCCCTAGCA GCCTGCCCTA CCTCTTTACC TGCTTCCTGG TG - #GAGTCAGG 540 - -
GATGTATACA TGAGCTGCTT TCCCTCTCAG CCAGAGGACA TGGGGGGCCC CA - #GCTCCCCT 600 - -
GCCTTTCCCC TTCTGTGCCT GGAGCTGGGA AGCAGGCCAG GGTTAGCTGA GG - #CTGGCTGG 660 - -
CAAGCAGCTG GGTGGTGCCA GGGAGAGCCT GCATAGTGCC AGGTGGTGCC TT - #GGGTTCCA 720 - -
AGCTAGTCCA TGGCCCCGAT AACCTTCTGC CTGTGCACAC ACCTGCCCCT CA - #CTCCACCC 780 - -
CCATCCTAGC TTTGGTATGG GGGAGAGGGC ACAGGGCCAG ACAAACCTGT GA - #GACTTTGG 840 - -
CTCCATCTCT GCAAAAGGGC GCTCTGTGAG TCAGCCTGCT CCCCTCCAGG CT - #TGCTCCTC 900 - - CCCC - #
- # - # 904 - - - - (2) INFORMATION FOR SEQ ID NO: 59: - - (i) SEQUENCE
CHARACTERISTICS: (A) LENGTH: 292 base - #pairs (B) TYPE: nucleic acid (C)
STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) - -
(iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID
NO: - #59: - - TTTTTTTGAG ACGGAGTCTT GCATCTGTCA TGCCCAGGCT GGAGTAGCAG TG - #GTGCCATC
60 - - TCGGCTCACT GCAAGCTCCA CCTCCCGAGT TCACGCCATT TTCCTGCCTC AG - #CCTCCCGA 120 - -
GTAGCTGGGA CTACAGGCGC CCGCCACCAT GCCCGGCTAA TTTTTTGTAT TT - #TTGGTAGA 180 - -
GACGGGGTTT CACCGTGTTA GCCAGAATGG TCTCGATCTC CTGACTTCGT GA - #TCCACCCG 240 - -
CCTCGGCCTC CCAAAGTTCT GGGATTACAG GTGTGAGCCA CCGCACCTGG CC - # 292 - - - - (2)
INFORMATION FOR SEQ ID NO: 60: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 262 base
- #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii)
MOLECULE TYPE: DNA (genomic) - - (iii) HYPOTHETICAL: NO

Detailed Description Paragraph Table (16):
- - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #60: - -
TTCTTTTTTG AGACAGGGTC TTGCTCTGTC ACCCAGGCCA GAGTGCAATG GT - #ACAGTCTC 60 - -
AGCTCACTGC AGCCTCAACC GCCTCGGCTC AAACCATCAT CCCATTTCAG CC - #TCCTGAGT 120 - -
AGCTGGGACT ACAGGCACAT GCCATTACAC CTGGCTAATT TTTTTGTATT TC - #TAGTAGAG 180 - -
ACAGGGTTTG GCCATGTTGC CCGGGCTGGT CTCGAACTCC TGGACTCAAG CA - #ATCCACCC 240 - -
ACCTCAGCCT CCCAAAATGA GG - # - # 262 - - - - (2) INFORMATION FOR SEQ ID NO: 61: - -
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 294 base - #pairs (B) TYPE: nucleic acid (C)
STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) - -
(iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID
NO: - #61: - - TTTTTTTTTG AGACAAACTT TCACTTTTGT TGCCCAGGCT GGAGTGCAAT GG - #CGCGATCT
60 - - CGGCTCACTG CAACCTCCAC CTCCCGGGTT CAAGTGATTC TCCTGCCTCA GC - #CTCTAGCC 120 - -
AAGTAGCTGC GATTACAGGC ATGCGCCACC ACGCCCGGCT AATTTTTGTA TT - #TTTAGTAG 180 - -
AGACGGGGTT TCGCCATGTT GGTCAGGCTG GTCTCGAACT CCTGATCTCA GG - #TGATCCAA 240 - -
CCACCCTGGC CTCCCAAAGT GCTGGGATTA TAGGCGTGAG CCACAGCGCC TG - #GC 294 - - - - (2)
INFORMATION FOR SEQ ID NO: 62: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base
- #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii)
MOLECULE TYPE: DNA (genomic) - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - -
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #62: - - TGACAGTCTC TCTGTCGCCC AGGCTGGAGT
GCAGTGGTGT GATCTTGGGT CA - #CTGCAACT 60 - - TCCGCCTCCC GGGTTCAAGG GATTCTCCTG
CCTCAGCTTC CTGAGTAGCT GG - #GGTTACAG 120 - - GTGTGTGCCA CCATGCCCAG CTAATTTTTT

TTTGTATTTT TAGTAGACAG GG - #TTTCACCA 180 - - TGTTGGTCAG GCTGGTCTCA AACTCCTGGC CTCAAGTGAT CCGCCTGACT CA - #GCCTACCA 240 - - AAGTGCTGAT TACAAGTGTG AGCCACCGTG CCCAGC - # - # 276 - - - - (2) INFORMATION FOR SEQ ID NO: 63: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 289 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #63: - - CGCCGGGCAC GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCAA GG - #CAGGTGGA 60 - - TCACGAGGTC AAGAGATCAA GACCATCCTG GCCAACATGG TGAAACCCCA TC - #TCTACTAA 120 - - AAATACGAAA AAATAGCCAG GCGTGGTGGC GGGTGCCTGT AATCCCAGCT AC - #TCGGGAGG 180 - - CTGAGGCAGG AGAATGGCAT GAACCCGGGA GGCAGAAGTT GCAGTGAGCC GA - #GATCGTGC 240 - - CACTGCACTC CAGCCTGGGC AACAGAGCGA GACTCTTGTC TCAAAAAAA - # 289 - - - - (2) INFORMATION FOR SEQ ID NO: 64: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 298 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #64: - - AGGCTGGGCT CTGTGGCTTA CGCCTATAAT CCCACCACGT TGGGAGGCTG AG - #GTGGGAGA 60 - - ATGGTTTGAG CCCAGGAGTT CAAGACAAGG CGGGGCAACA TAGTGTGACC CC - #ATCTCTAC 120 - - CAAAAAAACC CCAACAAAAC CAAAAATAGC CGGGCATGGT GGTATGCGGC CT - #AGTCCCAG 180 - - CTACTCAAGG AGGCTGAGGT GGGAAGATCG CTTGATTCCA GGAGTTTGAG AC - #TGCAGTGA 240 - - GCTATGATCC CACCACTGCC TACCATCTTT AGGATACATT TATTTATTTA TA - #AAAGAA 298 - - - - (2) INFORMATION FOR SEQ ID NO: 65: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #65: - - TTTTTTACAT CTTTAGTAGA GACAGGGTTT CACCATATTG GCCAGGCTGC TC - #TCAAACTC 60 - - CTGACCTTGT GATCCACCAG CCTCGGCCTC CCAAAGTGCT GGGAT - # 105 - - - - (2) INFORMATION FOR SEQ ID NO: 66: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 83 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) - - (iii) HYPOTHETICAL: NO - - (iv) ANTI-SENSE: NO - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #66: - - CCTCGAACTC CTAGGCTCAG GCAATCCTTT CACCTTAGCT TCTCAAAGCA CT - #GGGACTGT 60 - - AGGCATGAGC CACTGTGCCT GGC - # - # 83 - - - - (2) INFORMATION FOR SEQ ID NO: 67: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 5'- # donor consensus splice sequence - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #67: - - AGAAGGTAAG T - # - # - # 11 - - - - (2) INFORMATION FOR SEQ ID NO: 68: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 5'- # donor consensus splice sequence - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #68: - - TGGAGGTGAG A - # - # - # 11 - - - - (2) INFORMATION FOR SEQ ID NO: 69: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 5'- # donor consensus splice sequence - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #69: - - CAGTCGTGAG G - # - # - # 11 - - - - (2) INFORMATION FOR SEQ ID NO: 70: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 5'- # donor consensus splice sequence - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #70: - - CCGAGGTGAG C - # - # - # 11 - - - - (2) INFORMATION FOR SEQ ID NO: 71: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 5'- # donor consensus splice sequence - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #71: - - TGGAGGTACC A - # - # - # 11 - - - - (2) INFORMATION FOR SEQ ID NO: 72: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 5'- # donor consensus splice sequence - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #72: - - GGAAGGTCAG T - # - # - # 11 - - - - (2) INFORMATION FOR SEQ ID NO: 73: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 5'- # donor consensus splice sequence - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #73: - - AGCAGGTGGG C - # - # - # 11 - - - - (2) INFORMATION FOR SEQ ID NO: 74: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 5'- # donor consensus splice sequence - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #74: - - GCCAGGTACA G - # - # - # 11 - - - - (2) INFORMATION FOR SEQ ID NO: 75: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY:

linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 5'- # donor consensus splice sequence - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #75: - - TGCTGGTGAG T - # - # - # 11 - - - - (2) INFORMATION FOR SEQ ID NO: 76: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 5'- # donor consensus splice sequence - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #76: - - ATACAGGGGAT - # - # - # 11 - - - - (2) INFORMATION FOR SEQ ID NO: 77: - - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base - #pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear - - (ii) MOLECULE TYPE: DNA (genomic) (A) DESCRIPTION: 3'- # acceptor consensus splice sequence - - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: - #77: - - ATACAGGGGA T - # - # - # 11 - - - - (2) INFORMATION FOR SEQ ID NO: 78: - - (i) SEQUENCE CHARACTERISTICS:

WEST

Generate Collection | Print

Search Results - Record(s) 21 through 30 of 33 returned.

☐ 21. Document ID: US 5986176 A

L12: Entry 21 of 33 File: USPT Nov 16, 1999

US-PAT-NO: 5986176
DOCUMENT-IDENTIFIER: US 5986176 A

TITLE: Transgenic plants expressing biocidal proteins

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 22. Document ID: US 5981852 A

L12: Entry 22 of 33 File: USPT Nov 9, 1999

US-PAT-NO: 5981852
DOCUMENT-IDENTIFIER: US 5981852 A

TITLE: Modification of sucrose phosphate synthase in plants

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 23. Document ID: US 5981831 A

L12: Entry 23 of 33 File: USPT Nov 9, 1999

US-PAT-NO: 5981831
DOCUMENT-IDENTIFIER: US 5981831 A

TITLE: Exo-(1--4)-.beta.-D galactanase

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 24. Document ID: US 5981711 A

L12: Entry 24 of 33 File: USPT Nov 9, 1999

US-PAT-NO: 5981711
DOCUMENT-IDENTIFIER: US 5981711 A

TITLE: MN-specific antibodies and hybridomas

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 25. Document ID: US 5973135 A

L12: Entry 25 of 33 File: USPT Oct 26, 1999

US-PAT-NO: 5973135
DOCUMENT-IDENTIFIER: US 5973135 A

TITLE: DNA comprising plum pox virus and tomato spotted wilt virus cDNAS for disease resistance

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 26. Document ID: US 5972886 A

L12: Entry 26 of 33 File: USPT Oct 26, 1999

US-PAT-NO: 5972886
DOCUMENT-IDENTIFIER: US 5972886 A

TITLE: Megakaryocyte differentiation factor

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 27. Document ID: US 5972353 A

L12: Entry 27 of 33 File: USPT Oct 26, 1999

US-PAT-NO: 5972353
DOCUMENT-IDENTIFIER: US 5972353 A

TITLE: MN proteins, polypeptides, fusion proteins and fusion polypeptides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 28. Document ID: US 5959078 A

L12: Entry 28 of 33 File: USPT Sep 28, 1999

US-PAT-NO: 5959078
DOCUMENT-IDENTIFIER: US 5959078 A

TITLE: Isolated polysialyl transferases

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

29. Document ID: US 5955075 A

L12: Entry 29 of 33 File: USPT Sep 21, 1999

US-PAT-NO: 5955075
DOCUMENT-IDENTIFIER: US 5955075 A

TITLE: Method of inhibiting tumor growth using antibodies to MN protein

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

30. Document ID: US 5783666 A

L12: Entry 30 of 33 File: USPT Jul 21, 1998

US-PAT-NO: 5783666
DOCUMENT-IDENTIFIER: US 5783666 A

TITLE: APC (adenomatous polyosis coli) protein

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

Generate Collection | Print

Term	Documents
SIGNAL.USPT.	833577
SIGNALS.USPT.	654885
SEQUENCE.USPT.	466647
SEQUENCES.USPT.	122745
POLY.USPT.	153988
POLIES.USPT.	6
POLYS.USPT.	105
A.USPT.	6579161
AS.USPT.	2402821
ADDITI$5	0
ADDITI.USPT.	16
(L8 AND (SIGNAL SAME SEQUENCE SAME ADDITI$5 SAME (POLY ADJ "A"))).USPT.	33

There are more results than shown above. Click here to view the entire set.

Display Format: TI Change Format

Previous Page Next Page

WEST

Generate Collection Print

L12: Entry 32 of 33 File: USPT Jul 9, 1996

DOCUMENT-IDENTIFIER: US 5534438 A
TITLE: Process for isolating genes and the gene causative of Huntington's disease and differential 3' polyadenylation in the gene

Priority Application Year (1):
1993

Abstract Text (1):
The underlying genetic defect of Huntington disease (HD) has been mapped to chromosomal band 4.sub.p 16.3. Refined localization using recombinant HD chromosome analysis and allelic association analyses have identified two distinct candidate regions. Using a cDNA hybrid selection procedure, .alpha.-adducin has been mapped to the proximal 2.2 Mb 4D gene candidate region within 20 kb of D4S95. Several clones have been mapped within the minimal region containing the HD gene. The clones GT 70 and GT 149 are particularly useful in detecting changes in this portion of the gene of HD patients.

Brief Summary Text (9):
In order to facilitate a description of various embodiments of the invention, FIGS. 13 and 15 of the Drawings show DNA sequences of GT 70, GT 149 and UTR of HD 14, respectively. A detailed description of the drawings follow hereinafter.

Brief Summary Text (10):
Many aspects of the invention may be used to develop information respecting HD. Various clones of the HD gene and surrounding DNA sequences are valuable in gene diagnosis and family studies. According to an aspect of the invention, gene clones GT 70 and GT 149 are particularly useful in detecting changes or re-arrangements in the HD gene to determine patient's susceptibility to HD.

Brief Summary Text (11):
According to another aspect of the invention the HD gene includes cDNA clones GT 70 and GT 149, as shown in FIG. 13.

Brief Summary Text (12):
Another aspect of the present invention is a novel purified cDNA molecule having the sequence equivalent to GT 70.

Brief Summary Text (13):
Another aspect of the present invention is a novel purified cDNA molecule having the sequence equivalent to GT 149.

Drawing Description Text (14):
FIG. 4a. Mapping of transcriptional units within the HD candidate region. Overlapping regions with Yacs 353G6, 70D11 and 2A11 were used to define 5 separate genomic BINS. Yacs A187G12 and D102A10 were used to further refine BIN 3 into three separate compartments: A,B,C. GT clones were mapped by hybridization to digest Yac DNA and assigned to BINS accordingly. GT 44, 48 and 49 mapped to both A187G12 and D102A10, as well as 70D11. All of these clones were contained within a .lambda. phage (.lambda.GT48) isolated using GT 48 as a probe. .lambda.GT48 contains a HindIII polymorphism (*) detected by both GT 44 and GT 48. FIG. 4b. Yac mapping of GT 44, illustrating the HindIII polymorphism. FIG. 4c. GT 24 hybridizes only to 70D11 and D102A10 indicating its position within BIN 3C.

Drawing Description Text (17):
Northern blot analysis of GT clones. Examples of mRNAs detected with GT clones originating from the candidate HD region are shown. Total RNA from each cell line or tissue was prepared by standard procedures. The lanes represent RNA from the following sources: 1) Caco-2 intestinal cells, 1A) Caco-2 poly A.sup.+ RNA, 2) HL60 cells, 2A) HL60 Poly A.sup.+, 3) lymphoblasts, 4) fibroblasts, 5) liver, 6) Cos cells, 7) frontal cortex, 8) feral brain, 10) Caco-2 intestinal cells. RNA was separated on 1% agarose gels containing 0.6M formaldehyde and transferred onto DX (Amersham) membranes. The integrity of the RNA is shown by the ethidium bromide stained gel in the left upper panel. Clones were radiolabeled by random priming and hybridization and washing conditions were carried out as previously described. The size of the message detected with each clone is indicated in kilobases.

Drawing Description Text (19):
Genomic rearrangement in two families with HD. Southern blot analysis of Msp I digested genomic DNA probed with GT 48 revealed an altered band in 2 of 250. FIGS. 7a and 7b show co-segregation of the altered 1.7 kb Msp I fragment with all affected individuals in both families. FIG. 7c Southern blot analysis of genomic DNA from one affected individual from each family (lanes 1 and 2) and a control (lane C). Genomic DNA digested with a variety of enzymes and probed with GT 48 resulted in altered bands identical in the affected individuals from the two families.

Drawing Description Text (21):
Alu retrotransposition within the HD candidate region. Mapping of the genomic region around GT 48 in controls and the affected individuals, localized the rearrangement to the 1.2 kb HindlII fragment on .lambda.GT48 (boxed). The 1.2 kb Hind III fragment (SEQ ID NO:5) was subcloned, sequenced and PCR primers spanning the insertion site were derived. These primers (A:ATGTAATTGTTCACGACATGTGGC (SEQ ID NO:13), B:AAATAACATCCAGAATCTTCAGAT) (SEQ ID NO:14) generated a 118 base pair fragment in normal individuals (FIG. 8b lanes 6-9) and 460 base pair product in five affected individuals from both families (FIG. 8b lanes 1-5). The 460 base pair PCR product was subcloned (TA cloning, Invitrogen) and sequenced by ABI automated sequencing. The inserted sequence represents a full length Alu element (bold) and the insertion site is flanked by a 9 base pair direct repeat (underlined).

Drawing Description Text (23):
Physical Map between D4S95 and D4S182: Long range physical mapping localized GT 24, GT 48 and the .alpha.-adducin cDNA clone to the same 60 kb Not I fragment. Cosmids J7 and B7 were isolated from a chromosome 4 specific library with D4S182 and .alpha.-adducin cDNA respectively. .lambda.GT48 and .lambda.GT24 were isolated from a .lambda. phage library using their respective GT clones. .lambda.gt48 and .lambda.SS2 form a contig overlapping with cosmid B7. An oligonucleotide from the 5' UTR of adducin detected the D4S182 cosmid J7 as well as .lambda.GT24. By physical mapping GT 48 is approximately 20 kb from GT 24.

Drawing Description Text (27):
Assignment of cDNA fragments to BINs by hybridization to overlapping YAC clones in the proposed region for the Huntington disease gene (A). The physical intervals defined by overlapping regions of 10 YAC clones are indicated as BINs. Each cDNA fragment was hybridized to all or a subset of the overlapping YACs such that they could be assigned to the defined regions. Two cDNA fragments (B) GT 70 and (C) GT 48 are shown hybridized to overlapping YACs digested with HindIII.

Drawing Description Text (29):
RNA hybridization analysis of 5 retrieved cDNA fragments from the candidate region. An ethidium bromide stained gel is shown in the upper left panel. The clone names, their physical interval (BIN) assignment and the size of the mRNAs that were detected (in kilobases) are indicated. Hybridization to RNA from Caco-2 (intestinal), HL60, Lymphoblast, Fibroblast cell lines or from frontal cortex RNAs are shown. Part of the analysis with GT 70 has been shown previously, but sizes of the bands have been reassessed.

Drawing Description Text (31):
Sequence analysis of GT 70 and GT 149. Two of the retrieved clones detected a pair of

large transcripts by hybridization to RNA. These clones did not overlap and were mapped to adjacent physical intervals defined by the overlapping YACs. They contained multiple exons, demonstrated strong cross species conservation and upon sequencing analysis displayed significant coding potential (underlined). In the listings, the letter "n" designates an unidentified nucleotide.

Drawing Description Text (33):
An illustration of identified cDNAs and their nucleotide positions corresponding to the HD sequence, GT 63, 70 and 149 are the fragments of the gene initially identified by gene tracking.

Drawing Description Text (41):
A1. Hybridization of GT 70 to poly A.sup.+ RNA from fetal brain and CaCO-2 (intestinal) cell line and to total RNA from CaCO-2 and Hep G2 cell lines reveals 2 transcripts with the larger transcript most predominant in brain and the smaller more abundant in the cell lines.

Detailed Description Text (4):
In spite of the limitation of using only four tissue sources, the combined length of the transcripts detected with the GT clones contained within the 70D11 YAC comprising 450 kilobases of genomic DNA adds to greater than 30 kilobases, indicating that a minimum of 7% of genomic DNA in this region is transcribed. This corresponds to the overall expected proportion of transcribed sequence, but in all likelihood does not correspond to all the genes in this region.

Detailed Description Text (5):
A number of cDNA clones were obtained that did not detect mRNAs by analysing total RNA of the source tissues. However, sequence analysis and their hybridization patterns strongly suggested that these clones were portions of genes. For example, GT 133, in BIN 4, detects multiple exons on genomic DNA but did not detect a message in total RNA from the tissues tested.

Detailed Description Text (8):
Our strategy has been to initially use these GT clones to screen cDNA libraries and to screen DNA and RNA from many HD patients in an effort to further refine the assessment of candidate genes. In this light, GT 24 which detects a large transcript clone close to an Alu retrotransposition event deserved further investigation. GT clones showing multiple bands on southern blot hybridization with excellent coding potential also warranted further consideration. For example, the transcription unit detected by GT 70 which has excellent coding potential, detects several genomic fragments, sees two distinct RNA species and also detects DNA changes or rearrangements in patients with HD.

Detailed Description Text (9):
GT 149 also detects transcriptional units and which also has excellent coding potention. The two transcriptional units are the same as those detected by GT 70. The two distinct mRNA species have respectively molecular weights of 10.3 kb and 13.7 kb. Such identified forms of the mRNA are due to variations in the 340 untranslated region of the HD gene. It is believed that the larger transcript which is present in the human brain in significantly increased mounts and as derived from the HD gene including the UTR HD 14 is closely associated with Huntington's Disease. The 3' UTR of HD 14 provides a useful entity for detecting, analyzing and the prognosis of Huntington's Disease in humans due to the selective increased expression of this entity in the human brain.

Detailed Description Text (10):
A transcriptional map as described in more detail in the Examples and used to develop the strategy in locating GT 70, GT 149 and HD 14, is equally applicable to any other genomic region and will greatly assist in the search for any disease gene. Furthermore, by cloning the disease gene, the development of a detailed transcription map of a particular region allows further assessment of the possible regulatory inter-relationships between genes in that region. In addition, antisense RNA or DNA can be provided to bind specifically with the HD gene mRNA, thereby interrupting the precise molecular choreography which express the gene as a protein. The antisense material provides a very useful form of gene therapy to possibly arrest HD progression

in the brain and other tissue (J. J. Toulme et al. Gene Vol. 72, No. 1, pg. 51-58, December 1988).

Detailed Description Text (58):
Using a transcription map derived from the defined region we also obtained candidate genes for HD. To construct the map, three overlapping YACS were used which spanned the entire region of interest extending approximately 0.5 Mb proximal and distal from the D4S95 locus, the marker which most consistently shows non-random allelic association with HD. A total of 50 cDNA clones were isolated using direct cDNA selection. A total of 250 HD patients were screened with a series of cDNA clones (GT), one of which (GT 48) revealed an insertion of an Alu repetitive element in two families with identical DNA marker haplotypes on their HD chromosomes. In addition to complete segregation with HD in these two families, the insertion is not seen in 1000 control chromosomes in the general population. This includes 14/687 persons with an identical core haplotype suggesting a causal relationship between this rearrangement and HD. The insertion site is immediately adjacent to two overlapping transcriptional units including .alpha.-adducin and another which encodes for a 12 kb transcript.

Detailed Description Text (66):
In addition to refined physical mapping, the clones were also categorized into transcription units by cross-hybridization to each other and to RNA from a variety of tissues and cell lines. The results for seven GT clones are shown in FIG. 6 of the clones that were isolated from the 70D11 YAC, one group was found to correspond to the .alpha.-adducin message previously identified.sup.12.

Detailed Description Text (70):
We have screened for rearrangements with those GT clones that map to BIN 3. One GT clone, GT 48 detects an insertion of approximately 330 bp in 2 of 250 HD patients. This rearrangement segregated with HD in both families (FIG. 7a, 7b) and was seen in genomic DNA digested with multiple enzymes (FIG. 7c). Interestingly, in one of these families (FIG. 7A) recombination had placed the HD gene distal to D4S125 (FIG. 5).

Detailed Description Text (73):
Detailed restriction mapping localized this rearrangement to a 1.2 kb HindIII fragment which contained a portion of GT 48 (FIG. 8a). Sequence analysis of the rearrangement in both families demonstrated an insertion element of 331 base pairs which is a member of the Alu family of mobile repetitive elements. With primers flanking the insertion site, the inserted element could be detected using PCR (FIG. 8b).

Detailed Description Text (76):
As previously described, several GT clones allowed the identification of cDNA for the .alpha.-adducin gene.sup.12. The 3' UTR of .alpha.-adducin maps 20 kb telomeric to D4S95.sup.12 (FIG. 9). An oligonucleotide primer which spans nucleotide 38-58 in the 5' untranslated region of the .alpha.-adducin gene maps telomeric to the Alu insertion and is located on the same 7.4 kb EcoRI fragment as GT 24 but does not hybridize to GT 24 (FIG. 9). In addition, a 501 bp RT-PCR product corresponding to nucleotides 38-539 of the .alpha.-adducin cDNA also detected the 7.4 kb EcoRI fragment. This places the 5' UTR of the .alpha.-adducin gene in close proximity to D4S182, flanking GT 24 and indicates that the .alpha.-adducin gene spans at least 80 kb between D4S95 and D4S182 (FIG. 9).

Detailed Description Text (78):
Corresponding transcript(s) for GT 48 and the two other adjacent clones, GT 44 and GT 49, were not detected. Northern blot analysis and screening of 10 different cDNA libraries with these cDNA clones did not yield any positive results. Sequence analysis of the 1.2 kb HindIII fragment containing GT 48 did not reveal a significant coding potential.

Detailed Description Text (79):
Nevertheless, the presence of a new Alu element might interfere with expression of other genes near the site of insertion. We therefore focused our attention on two other cDNA clones. GT 24 and GT 34. Northern blot analysis showed that GT 34 detected a 4 kb transcript in a variety of tissues including brain, lymphoblasts and fibroblasts. A 4 kb cDNA clone (cD510) was then isolated with GT 34 as probe. Sequence analysis of this cDNA clone revealed no homology with sequences in Genbank. Further

mapping data showed that the genomic DNA sequence corresponding to cD510 mapped distal to D4S95, but centromeric to the 3' UTR of .alpha.-adducin and at least 70 kb from the site of the Alu insertion (FIG. 4). Based on the map location, therefore, cD510 became an unlikely candidate for the HD gene.

Detailed Description Text (80):
The third clone, GT 24, was mapped approximately 20 kb from GT 48 (FIG. 9). Although GT 24 is also contained in an intron of the .alpha.-adducin gene it detected a different transcript of 12 kb (FIG. 4, FIG. 6) in many tissues including frontal cortex, fibroblasts, lymphoblasts, and intestinal cells (CaCO2). Besides some weak identity with the LINE-1 element, this clone also has no homology with any sequence in the data bases. However, at 69 bp open reading frame flanked by appropriate splice junctions was noted.sup.23. Furthermore, based on its map position close to the Alu insertion site, the 12 kb transcript is a candidate gene for HD.

Detailed Description Text (96):
Manual or automated (ABI 373A) sequence data were obtained and entered into a Sun Microsystems Sparc IPX workstation and compared with previously entered sequence data (of GT clones) using the XDAP module of the Staden package. Sequence data were then sent to the e-mail server at the National Center for Biotechnology Information (NCBI) and compared with the non-redundant GenBank, dbEST, Macvector and Transcription Factor databases using the BLAST suite of programs. The CRM module of the Gene Recognition Analysis Internet Link (GRAIL) e-mail server was used to assess protein-coding potential and a search for open reading frames bracketed by splice junctions was conducted with the SORFIND program. The PYTHIA e-mail server was used to identify and classify known human repeat elements.

Detailed Description Text (102):
A series of additional overlapping YACs were also used to define physical intervals or BINs across the 1 megabase region as depicted in FIG. 11A. Refined positioning of each cDNA was deduced by the hybridization pattern to this array of YACs. For example, the hybridization pattern of clone GT70 (FIG. IIB) is consistent with it originating from the overlapping portions of the 353G6 and 70D11 YACs, in BIN 2. As well, this clone detected multiple bands indicating that it contains more than a single exon and also displayed striking cross species hybridization. The GT 48 clone (FIG. 11C) detected two HindIII restriction fragments in three of the YACs suggesting it originates from BIN 3B. It detected only a single EcoRI genomic fragment and did not show cross species hybridization. An additional 56 clones were mapped in a similar manner and the results are listed in Table 3.

Detailed Description Text (103):
Refined map position was obtained for two cDNA fragments which were located at the ends of the 70D11 YAC. The hybridization pattern seen with GT 70 on the different YACs (FIG. 11B) and chromosome 4 hybrid and human DNAs, (data not shown) indicate that this clone in all likelihood maps to the end of the human DNA segment in the 70D11 YAC and is entirely contained within the other YACs to which it hybridized including 33306. Through a similar analysis the clone GT 133 from BIN 4 was found to originate from the other end of the 70D11 YAC.

Detailed Description Text (106):
The combined information of RNA hybridization and physical mapping clearly indicate that some of the GT clones were portions of the same transcription units. GT 70 and GT 149 (FIG. 12), for example, both detect the same distinct pair of very large transcripts (10 and 12 kilobases). Furthermore, GT 70 and GT 149 map close to each other (FIG. 11 and Table 3), but they do not cross-hybridize nor overlap by sequence analysis. Both GT 70 and GT 149 have excellent coding potential as judged by the GRAIL e-mail server (FIG. 13 and Table 3). Furthermore, GT 63 hybridized to EcoRI fragments that were identical in size to those detected by GT 70 and was found by cross-hybridization to overlap with it (Table 3).

Detailed Description Text (108):
Overlapping clones were found by cross-hybridization of individual clones to all others or by sequence analysis. For example, GT 98 which detects a 3.6 Kb transcript hybridized to two other clones in BIN 5 (Table 3). One of these, GT 123, is also located in BIN 5 but only weakly cross-hybridized to GT 98 and does detect a

transcript of identical size. That these clones overlap was also supported by examining the EcoRI genomic restriction fragments to which these clones hybridized (Table 3).

Detailed Description Text (109):
Sequencing indicated the majority of clones selected were independently derived. Some of the overlapping clones (Table 3) detected abundant mRNAs. An exception was noted for GT 23 of BIN 3 which was derived from frontal cortex cDNA, did not detect mRNA and yet showed overlap with five other clones of 100 examined. It also hybridized to clones originating from fetal brain cDNA from a different selection experiment. Cross hybridization did not occur from repetitive sequence, as all of these clones hybridized to a single EcoRI band in genomic DNAs. This does suggest a preferential selection of this sequence through the process of hybridization to the immobilized genomic DNA or during amplification of the retrieved material. This preference was not evident with the tissue mix cDNA selection as GT 23 detected only two clones (both of which were not characterized further) of 100 tested, indicating that selection with a wider diversity of starting cDNAs may minimize the preferential retrieval of some sequences.

Detailed Description Text (110):
In addition to the patterns of DNA and RNA hybridization, sequence analysis was performed to determine cDNA overlap, their coding potential and to search databases of sequenced genes for identity or similarity. Many clones appeared to have been derived from unprocessed RNA since they lacked consistent open reading frames. Potential or partial exons were detected in them using the SORFIND program. Out of 31 non-overlapping clones, 5 showed identity with .alpha.-adducin and one, GT 161, was identical with the expressed sequence tag HUMXT01095.

Detailed Description Text (111):
One cDNA fragment appeared to detect additional sequences. For example, GT 161 which showed identity to an expressed sequence tag, hybridized strongly to the 2A11 YAC DNA digested with EcoRI and to a band of corresponding size in total human DNA (Table 3). A less prominent hybridizing band was also observed in human DNA that corresponded in intensity and size to one seen in a human-hamster hybrid containing chromosome 1 as its only human material, suggesting this clone represents a portion of a gene which may belong to a gene family (Table 3).

Detailed Description Text (127):
A combination of general purpose text processing software and local sequence analysis software was used to extract subsets of the large public data bases based on feature table entries for poly A sites and for 3' UTR regions. These subset data bases were searched using a complete dynamic programming algorithm.

Detailed Description Text (132):
As part of our strategy to detect the transcriptional units originating from the region spanning 500 kb on either side of the D4S95 locus, we previously isolated 58 cDNA segments. Three of the CDNA clones (GT 149, GT 63 and GT 70) (FIG. 14) were found to correspond to the sequence of the HD gene. Using two of these nonoverlapping cDNAs (GT 70 and GT 149), we screened a human frontal cortex cDNA library and identified two larger cDNA clones (cD 70-2 and HD 149-101) (FIG. 14). HD 149-101 and cD 70-2 were used to screen a number of other human cDNA libraries including those of retina, frontal cortex, fetal brain, caudate, and muscle tissues. In addition, a 1 kb PCR product corresponding to nucleotide 8000-9000 of the published sequence, was also used to screen the frontal cortex library. Additional cDNAs were identified including HD 12 and HD 14.

Detailed Description Text (138):
GT 70, GT 149 and cD 70-2 detected two mRNA transcripts in all tissues assessed including total and/or poly A.sup.+ RNA from lymphoblast, frontal cortex (FIG. 17), intestine, liver and lung (data not shown). Similarly two transcripts were seen in total and poly A.sup.+ RNA from a number of cell lines including lymphoblast, CaCO-2, Hep G2 (FIG. 17), HL 60 and 293S cells (data not shown) (FIG. 17). Using conditions that discriminated between human and rodent transcripts, these mRNAs were also both observed (data not shown) in the hybrid cell line GM 10115 containing chromosome 4 as its only human component indicating that both transcripts originate from chromosome 4.

Furthermore all hybridizing genomic bands detected by these cDNA fragments could be accounted for between total human, chromosome 4 and YAC DNA (data not shown). This information provides further evidence that the two messages in all likelihood correspond to a single HD gene.

Detailed Description Text (139):
The larger mRNA is the predominant transcript in adult and fetal human brain compared to lymphoblasts and cell lines including Hep G2 and CaCO-2 where the smaller sized transcript is more abundant (FIG. 17). This was confirmed by densitometry analysis which showed a decreased intensity of approximately 3 fold in the ratio of the smaller to the larger transcript in adult and fetal brain. In contrast, in lymphoblast and cell lines as noted and in human intestines, liver and lung, the smaller to larger transcript ratio was increased in intensity by at least 2 fold. The non overlapping 2.4 kb HindIII and 1.4 PstI/EcoRI fragments of HD 14 were used in Northern Blot analysis and in contrast to the two transcripts detected with GT 70, GT 149 and cD 70-2, only the single larger 13.7 kb mRNA was detected (FIG. 17).

Detailed Description Text (140):
The earlier finding that the GT 70 and GT 149 corresponding to the HD gene detected two different sized mRNA species (Experiment 3) prompted an investigation of the relationship between these two mRNA species. We uncovered partially overlapping but distinct cDNA clones which span 4164 bp (HD 12) and 5,710 bp (HD 14) respectively. The region of overlap between these two cDNAs and the HD sequence shows an identical protein coding sequence, but in HD 14 an additional 3,360 bp of non-coding sequence is identified.

Detailed Description Text (141):
This experiment demonstrates that the identified cDNAs (HD 12 and HD 14) originate from a single gene by DNA-hybridization analysis, restriction mapping and sequencing. Several mechanisms can lead to generation of different mRNAs from the same gene. Differential splicing events, alternate use of transcription start sites, or the selection of different polyadenylation sites can lead to multiple mRNA species generated from the same genomic region. Our experiments show that differential polyadenylation results in a larger transcript detected by RNA hybridization. It is generally appreciated that the majority of eukaryotic mRNAs possess a poly A tract at their 3' terminus. The addition of poly A occurs post-transcriptionally in the nucleus and involves cleavage of the primary transcript and subsequent addition of poly A to the newly formed 3' end. The cis-acting sequence usually AATAAA, located 15-25 nucleotides upstream of the poly A addition site, is highly conserved and critical for polyadenylation. Alterations within these cis-acting sequences can lead to the reduction or even abolition of 3' processing. Both the hexanucleotides seen in the HD 12 and HD 14 cDNAs have substitutions within this consensus that would be predicted to reduce the cleavage of the primary transcript and subsequent addition of poly A to the newly formed 3' end. The AGTAAA hexanucleotide which is seen 5' of the poly A tail on the HD 12 cDNA would be predicted to have significantly less (.about.30%) efficacy in affecting cleavage and subsequent addition of poly A compared to mRNA with the complete sequence AATAAA and yet for most issues excluding brain this appears to be the predominantly used signal. The hexanucleotide ATTAAA which is seen 5' to the poly A of the larger cDNA (HD 14) is predicted to more efficient relative to AGTAAA but also would be predicted to have less (.about.70%) efficacy for processing and addition of poly A to the newly formed 3' end than the consensus sequence.

Detailed Description Text (147):
It is also, of course, possible to express genes encoding polypeptides in eukaryotic host cell cultures derived from multicellular organisms. Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including HeLa cells, Chinese hamster ovary (CHO) cells, baby hamster kidney (BHK) cells, and a number of other cell lines. Suitable promoters for mammalian cells are also known in the art and include viral (1978), Rous sarcoma virus (RSV), adenovirus (ADV), and bovine papilloma virus (BPV). Mammalian cells may also require terminator sequences and poly A addition sequences; enhancer sequences which increase expression may also be included, and sequences which cause amplification of the gene may also be desirable. These sequences are known in the art. Vectors suitable for replication in mammalian cells may include viral replicons, or sequences which insure integration of

the appropriate sequences encoding NANBV epitope into the host genome.

Detailed Description Paragraph Table (3):

TABLE 3

Clone EcoRI Frag RNA Hybridization GT Size (bp) Sizes Size and Distribution Sequence Analysis

BIN 1A BIN 1B ##STR1## -650 -600 912 7.0 12.0 12.0 5.5 kb: W, Fl, C, B, Co absent absent ##STR2## 65 207 2.9 absent DB search neg. 69 976 3.8 absent DB search neg. MER3c repeat, 12 bpGT repeat ##STR3## 573 -500 -600 9.5 9.5 9.0 absent absent ##STR4## 166 -550 12.0 4.5 kb: similar to GT88 Not sequenced 88 -600 6.0 4.5 kb: similar to GT 166 Not sequenced 149 584 6.0, 5.0 10 kb, 12 kb: K, Co, Fi, L, W, C DB search neg. Coding Potential Excellent, Predicted exon. BIN 2 66 165 644 600; 550 10.0 11.5, 4.2 absent absent ##STR5## 87 536 8.5 absent DB search neg. 70 63 757 600 9.0, 8.5, 1.2 9.0, 1.2 10.0, 12.0 kb,: L, F, C, W, B ND ##STR6## 54 757 2.7 absent DB search neg. ALU and MER18 repeats 72 764 2.8 absent DB search neg. 189 695; 578 11.0, 6.0 DB search neg. 2 partial ALU repeats, composite clone BIN 3A BIN 3B ##STR7## 551 592 532 595 589 597 14.0 14.0 14.0 14.0 absent absent ##STR8## 136 -500 14.0, 7.5 absent Not sequenced 44 646 13.7 absent DB search neg. 48 550 14.0 absent DB search neg. ##STR9## 516 -500 560 9.0 5.0 3.8 kb: W, L, F, C, Co ND ##STR10## 167 -500 6.4 absent Not sequenced. ##STR11## 490 -600 -500 -560 -450 13.0 15.0 7.0 14.0, 2.8, 0.5 10.0, 5.2 4.0 kb: Adducin 4.0 kb: Adducin 4.0 kb: Adducin 4.0 kb: Adducin 4.0 kb: Adducin 24 -600 15.0, 7.8, 6.0 12.0 kb DB search neg. 307 bp similar to LI repeat. 30 458 6.0 DB search neg. ALU repeat 138 -600 13.0 absent DB similarity, 4.2e-4, HSILIAG, Alu repeat present ##STR12## -550 550 8.0, 14.0 16.0, 14.0, 7.5 14.0 ND absent absent ##STR13## 53 -550 16.0 absent DB search neg. 182 bp of L1 repeat BIN4 128 480 14.0 absent DB search neg ##STR14## 422 443:250 439 400 12.0.11.0 11.0.9.0.4.2 11.0 5.5 kb 5.5 kb 5.5 kb ##STR15## 43 495 6.0 absent DB search neg. 495 bp ORF. coding potential 133 480 14.0.18.0 absent DB search neg. BIN 3A BIN 5b ##STR16## 450 447 352 14.0.9.0 14.0.9.0.4.1 14.0.9.0 3.6 kb: wide distribution 1.8,3.6 kb: FI, L, W, C, C o ND ##STR17## 125 662 7.5 absent DB search neg. 137 500 9.0 absent DB search neg. 160 -500 4.2 absent DB search neg (partial sequence). 179 bp ORF. Coding potential good. 161 349 9.0 3.8 kb: DB match, 3.3e-102,HUMXT01095 (EST) is identical

Table 3

Legend Summary of characterization of 58 retrieved cDNA fragments. The clones ar listed by name (as GTnos.) according to their physical intervals or BINs assignment YAC clones. The sizes of the cDNA fragments are given in base pairs. The genomic fragments detected with these clones in human and yeas DNAs digested with EcoRI are also listed. Sizes of mRNAs detected in the tissues are given in kilobases from K--Kidney, Co--Cos cells, Fi--fibroblasts, L--lymphoblast, W--HL60 cells, C--Cacp2 cells, B--bone marrow, F--frontal cortex, FB--fetal brain. Groups of clones that are shown bracketed indicate those that partially overlap as determined by cross hybrodization or sequence analysis. Database (DB) searches were carried out against nonredundant nucleic acid and protein databases of NCBI, as well as the dbEST and Transcription Factor databases. Characterized repeat sequences were edited prior to BLAST searches. All database marches with BLAST expectation values less than 1 .times. 10.sup.-4 are reported, but similarities greater than 10.sup.-10 were considered borderline. Coding potential was judged by the GRAIL email server and potential exons were identified using the SORFIND program. Human repeat sequences were identified by the PYTHIA email server.

WEST

Generate Collection | Print

Search Results - Record(s) 31 through 33 of 33 returned.

☐ 31. Document ID: US 5648212 A

L12: Entry 31 of 33 File: USPT Jul 15, 1997

US-PAT-NO: 5648212
DOCUMENT-IDENTIFIER: US 5648212 A

TITLE: Detection of inherited and somatic mutations of APC gene in colorectal cancer of humans

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 32. Document ID: US 5534438 A

L12: Entry 32 of 33 File: USPT Jul 9, 1996

US-PAT-NO: 5534438
DOCUMENT-IDENTIFIER: US 5534438 A

TITLE: Process for isolating genes and the gene causative of Huntington's disease and differential 3' polyadenylation in the gene

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 33. Document ID: US 5352775 A

L12: Entry 33 of 33 File: USPT Oct 4, 1994

US-PAT-NO: 5352775
DOCUMENT-IDENTIFIER: US 5352775 A

TITLE: APC gene and nucleic acid probes derived therefrom

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

Generate Collection | Print

Term	Documents
SIGNAL.USPT.	833577
SIGNALS.USPT.	654885
SEQUENCE.USPT.	466647
SEQUENCES.USPT.	122745
POLY.USPT.	153988
POLIES.USPT.	6
POLYS.USPT.	105
A.USPT.	6579161
AS.USPT.	2402821
ADDITI$5	0
ADDITI.USPT.	16
(L8 AND (SIGNAL SAME SEQUENCE SAME ADDITI$5 SAME (POLY ADJ "A"))).USPT.	33

There are more results than shown above. Click here to view the entire set.

Display Format: TI Change Format

Previous Page Next Page

WEST

Generate Collection | Print

Search Results - Record(s) 1 through 10 of 39 returned.

1. Document ID: US 6475480 B1

L22: Entry 1 of 39 File: USPT Nov 5, 2002

US-PAT-NO: 6475480
DOCUMENT-IDENTIFIER: US 6475480 B1

TITLE: Use of adenoviral E4 reading frames to improve expression of a gene of interest

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

2. Document ID: US 6391565 B2

L22: Entry 2 of 39 File: USPT May 21, 2002

US-PAT-NO: 6391565
DOCUMENT-IDENTIFIER: US 6391565 B2

TITLE: Methods of detecting growth differentiation factor-3

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

3. Document ID: US 6380463 B1

L22: Entry 3 of 39 File: USPT Apr 30, 2002

US-PAT-NO: 6380463
DOCUMENT-IDENTIFIER: US 6380463 B1

TITLE: Inducible herbicide resistance

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

4. Document ID: US 6338850 B1

L22: Entry 4 of 39 File: USPT Jan 15, 2002

US-PAT-NO: 6338850
DOCUMENT-IDENTIFIER: US 6338850 B1

TITLE: Methods and products for controlling the immune response of a mammal to glutamic acid decarboxylase

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 5. Document ID: US 6312683 B1

L22: Entry 5 of 39 File: USPT Nov 6, 2001

US-PAT-NO: 6312683
DOCUMENT-IDENTIFIER: US 6312683 B1

TITLE: Equine infectious anemia virus vectors

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 6. Document ID: US 6303313 B1

L22: Entry 6 of 39 File: USPT Oct 16, 2001

US-PAT-NO: 6303313
DOCUMENT-IDENTIFIER: US 6303313 B1

TITLE: Method for generating libraries of antibody genes comprising amplification of diverse antibody DNAs and methods for using these libraries for the production of diverse antigen combining molecules

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 7. Document ID: US 6297429 B1

L22: Entry 7 of 39 File: USPT Oct 2, 2001

US-PAT-NO: 6297429
DOCUMENT-IDENTIFIER: US 6297429 B1

TITLE: Gene for transcription factor capable of altering characters of a plant and use thereof

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 8. Document ID: US 6297028 B1

L22: Entry 8 of 39 File: USPT Oct 2, 2001

US-PAT-NO: 6297028
DOCUMENT-IDENTIFIER: US 6297028 B1

TITLE: IL-2R-associated polypeptide and DNA molecules coding therefor

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 9. Document ID: US 6297017 B1

L22: Entry 9 of 39 File: USPT Oct 2, 2001

US-PAT-NO: 6297017
DOCUMENT-IDENTIFIER: US 6297017 B1

TITLE: Categorising nucleic acids

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 10. Document ID: US 6265634 B1

L22: Entry 10 of 39 File: USPT Jul 24, 2001

US-PAT-NO: 6265634
DOCUMENT-IDENTIFIER: US 6265634 B1

TITLE: Polyribozyme capable of conferring on plants resistance to cucumber mosaic virus and resistant plants producing this polyribozyme

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

Generate Collection | Print

Term	Documents
SITE.USPT.	230237
SITES.USPT.	149027
SIGNAL.USPT.	833577
SIGNALS.USPT.	654885
TERMINAT$	0
TERMINAT.USPT.	22
TERMINATABILITY.USPT.	1
TERMINATABLE.USPT.	56
TERMINATAES.USPT.	3
TERMINATAL.USPT.	3
TERMINATAR/POLYADENYLATION.USPT.	1
(L21 AND (TERMINAT$ SAME (SITE OR SIGNAL) SAME (DELETE$ OR MUTAT$ OR REMOV$ OR ELIMINAT$))).USPT.	39

There are more results than shown above. Click here to view the entire set.

Display Format: TI Change Format

Previous Page Next Page

WEST

Generate Collection | Print

Search Results - Record(s) 1 through 10 of 39 returned.

1. Document ID: US 6475480 B1

L22: Entry 1 of 39 File: USPT Nov 5, 2002

US-PAT-NO: 6475480
DOCUMENT-IDENTIFIER: US 6475480 B1

TITLE: Use of adenoviral E4 reading frames to improve expression of a gene of interest

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

2. Document ID: US 6391565 B2

L22: Entry 2 of 39 File: USPT May 21, 2002

US-PAT-NO: 6391565
DOCUMENT-IDENTIFIER: US 6391565 B2

TITLE: Methods of detecting growth differentiation factor-3

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

3. Document ID: US 6380463 B1

L22: Entry 3 of 39 File: USPT Apr 30, 2002

US-PAT-NO: 6380463
DOCUMENT-IDENTIFIER: US 6380463 B1

TITLE: Inducible herbicide resistance

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc
Image

4. Document ID: US 6338850 B1

L22: Entry 4 of 39 File: USPT Jan 15, 2002

US-PAT-NO: 6338850
DOCUMENT-IDENTIFIER: US 6338850 B1

TITLE: Methods and products for controlling the immune response of a mammal to glutamic acid decarboxylase

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 5. Document ID: US 6312683 B1

L22: Entry 5 of 39 File: USPT Nov 6, 2001

US-PAT-NO: 6312683
DOCUMENT-IDENTIFIER: US 6312683 B1

TITLE: Equine infectious anemia virus vectors

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 6. Document ID: US 6303313 B1

L22: Entry 6 of 39 File: USPT Oct 16, 2001

US-PAT-NO: 6303313
DOCUMENT-IDENTIFIER: US 6303313 B1

TITLE: Method for generating libraries of antibody genes comprising amplification of diverse antibody DNAs and methods for using these libraries for the production of diverse antigen combining molecules

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 7. Document ID: US 6297429 B1

L22: Entry 7 of 39 File: USPT Oct 2, 2001

US-PAT-NO: 6297429
DOCUMENT-IDENTIFIER: US 6297429 B1

TITLE: Gene for transcription factor capable of altering characters of a plant and use thereof

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 8. Document ID: US 6297028 B1

L22: Entry 8 of 39 File: USPT Oct 2, 2001

US-PAT-NO: 6297028
DOCUMENT-IDENTIFIER: US 6297028 B1

TITLE: IL-2R-associated polypeptide and DNA molecules coding therefor

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 9. Document ID: US 6297017 B1

L22: Entry 9 of 39 File: USPT Oct 2, 2001

US-PAT-NO: 6297017
DOCUMENT-IDENTIFIER: US 6297017 B1

TITLE: Categorising nucleic acids

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 10. Document ID: US 6265634 B1

L22: Entry 10 of 39 File: USPT Jul 24, 2001

US-PAT-NO: 6265634
DOCUMENT-IDENTIFIER: US 6265634 B1

TITLE: Polyribozyme capable of conferring on plants resistance to cucumber mosaic virus and resistant plants producing this polyribozyme

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

Generate Collection | Print

Term	Documents
SITE.USPT.	230237
SITES.USPT.	149027
SIGNAL.USPT.	833577
SIGNALS.USPT.	654885
TERMINAT$	0
TERMINAT.USPT.	22
TERMINATABILITY.USPT.	1
TERMINATABLE.USPT.	56
TERMINATAES.USPT.	3
TERMINATAL.USPT.	3
TERMINATAR/POLYADENYLATION.USPT.	1
(L21 AND (TERMINAT$ SAME (SITE OR SIGNAL) SAME (DELETE$ OR MUTAT$ OR REMOV$ OR ELIMINAT$))).USPT.	39

There are more results than shown above. Click here to view the entire set.

Display Format: TI Change Format

Previous Page Next Page

WEST

Generate Collection | Print

Search Results - Record(s) 11 through 20 of 39 returned.

☐ 11. Document ID: US 6258769 B1

L22: Entry 11 of 39 File: USPT Jul 10, 2001

US-PAT-NO: 6258769
DOCUMENT-IDENTIFIER: US 6258769 B1

TITLE: Peroxidase variants with improved hydrogen peroxide stability

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 12. Document ID: US 6177075 B1

L22: Entry 12 of 39 File: USPT Jan 23, 2001

US-PAT-NO: 6177075
DOCUMENT-IDENTIFIER: US 6177075 B1

TITLE: Insect viruses and their uses in protecting plants

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 13. Document ID: US 6147280 A

L22: Entry 13 of 39 File: USPT Nov 14, 2000

US-PAT-NO: 6147280
DOCUMENT-IDENTIFIER: US 6147280 A

TITLE: Production of oligosaccharides in transgenic plants

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 14. Document ID: US 6080920 A

L22: Entry 14 of 39 File: USPT Jun 27, 2000

US-PAT-NO: 6080920
DOCUMENT-IDENTIFIER: US 6080920 A

TITLE: Transgenic plants exhibiting altered flower color and methods for producing

same

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 15. Document ID: US 6077994 A

L22: Entry 15 of 39 File: USPT Jun 20, 2000

US-PAT-NO: 6077994
DOCUMENT-IDENTIFIER: US 6077994 A

TITLE: Genetic control of flowering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 16. Document ID: US 6075138 A

L22: Entry 16 of 39 File: USPT Jun 13, 2000

US-PAT-NO: 6075138
DOCUMENT-IDENTIFIER: US 6075138 A

TITLE: Transcriptional regulatory DNA sequence elements and signal peptide sequence of the Coriolus hirsutus phenoloxidase gene, and plasmid vectors and transformants utilizing such sequences

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 17. Document ID: US 6066491 A

L22: Entry 17 of 39 File: USPT May 23, 2000

US-PAT-NO: 6066491
DOCUMENT-IDENTIFIER: US 6066491 A

TITLE: Process for obtaining fungal resistant plants with recombinant polynucleotides encoding .beta.-1,3-glucanase modified for apoplast targeting

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 18. Document ID: US 6028250 A

L22: Entry 18 of 39 File: USPT Feb 22, 2000

US-PAT-NO: 6028250
DOCUMENT-IDENTIFIER: US 6028250 A

TITLE: Plant promoter and method for gene expression using said promoter

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

☐ 19. Document ID: US 6018103 A

L22: Entry 19 of 39 File: USPT Jan 25, 2000

US-PAT-NO: 6018103
DOCUMENT-IDENTIFIER: US 6018103 A

TITLE: Chimeric plant genes possessing independent regulatory sequences

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

☐ 20. Document ID: US 5998697 A

L22: Entry 20 of 39 File: USPT Dec 7, 1999

US-PAT-NO: 5998697
DOCUMENT-IDENTIFIER: US 5998697 A

TITLE: Transgenic fish and vectors therefor

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

Generate Collection | Print

Term	Documents
SITE.USPT.	230237
SITES.USPT.	149027
SIGNAL.USPT.	833577
SIGNALS.USPT.	654885
TERMINAT$	0
TERMINAT.USPT.	22
TERMINATABILITY.USPT.	1
TERMINATABLE.USPT.	56
TERMINATAES.USPT.	3
TERMINATAL.USPT.	3
TERMINATAR/POLYADENYLATION.USPT.	1
(L21 AND (TERMINAT$ SAME (SITE OR SIGNAL) SAME (DELETE$ OR MUTAT$ OR REMOV$ OR ELIMINAT$))).USPT.	39

There are more results than shown above. Click here to view the entire set.

Display Format: TI Change Format

Previous Page Next Page

WEST

Generate Collection | Print

Search Results - Record(s) 11 through 20 of 39 returned.

11. Document ID: US 6258769 B1

L22: Entry 11 of 39 File: USPT Jul 10, 2001

US-PAT-NO: 6258769
DOCUMENT-IDENTIFIER: US 6258769 B1

TITLE: Peroxidase variants with improved hydrogen peroxide stability

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

12. Document ID: US 6177075 B1

L22: Entry 12 of 39 File: USPT Jan 23, 2001

US-PAT-NO: 6177075
DOCUMENT-IDENTIFIER: US 6177075 B1

TITLE: Insect viruses and their uses in protecting plants

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

13. Document ID: US 6147280 A

L22: Entry 13 of 39 File: USPT Nov 14, 2000

US-PAT-NO: 6147280
DOCUMENT-IDENTIFIER: US 6147280 A

TITLE: Production of oligosaccharides in transgenic plants

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

14. Document ID: US 6080920 A

L22: Entry 14 of 39 File: USPT Jun 27, 2000

US-PAT-NO: 6080920
DOCUMENT-IDENTIFIER: US 6080920 A

TITLE: Transgenic plants exhibiting altered flower color and methods for producing

same

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 15. Document ID: US 6077994 A

L22: Entry 15 of 39 File: USPT Jun 20, 2000

US-PAT-NO: 6077994
DOCUMENT-IDENTIFIER: US 6077994 A

TITLE: Genetic control of flowering

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 16. Document ID: US 6075138 A

L22: Entry 16 of 39 File: USPT Jun 13, 2000

US-PAT-NO: 6075138
DOCUMENT-IDENTIFIER: US 6075138 A

TITLE: Transcriptional regulatory DNA sequence elements and signal peptide sequence of the Coriolus hirsutus phenoloxidase gene, and plasmid vectors and transformants utilizing such sequences

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 17. Document ID: US 6066491 A

L22: Entry 17 of 39 File: USPT May 23, 2000

US-PAT-NO: 6066491
DOCUMENT-IDENTIFIER: US 6066491 A

TITLE: Process for obtaining fungal resistant plants with recombinant polynucleotides encoding .beta.-1,3-glucanase modified for apoplast targeting

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

---

☐ 18. Document ID: US 6028250 A

L22: Entry 18 of 39 File: USPT Feb 22, 2000

US-PAT-NO: 6028250
DOCUMENT-IDENTIFIER: US 6028250 A

TITLE: Plant promoter and method for gene expression using said promoter

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

19. Document ID: US 6018103 A

L22: Entry 19 of 39 File: USPT Jan 25, 2000

US-PAT-NO: 6018103
DOCUMENT-IDENTIFIER: US 6018103 A

TITLE: Chimeric plant genes possessing independent regulatory sequences

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

20. Document ID: US 5998697 A

L22: Entry 20 of 39 File: USPT Dec 7, 1999

US-PAT-NO: 5998697
DOCUMENT-IDENTIFIER: US 5998697 A

TITLE: Transgenic fish and vectors therefor

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

Generate Collection | Print

Term	Documents
SITE.USPT.	230237
SITES.USPT.	149027
SIGNAL.USPT.	833577
SIGNALS.USPT.	654885
TERMINAT$	0
TERMINAT.USPT.	22
TERMINATABILITY.USPT.	1
TERMINATABLE.USPT.	56
TERMINATAES.USPT.	3
TERMINATAL.USPT.	3
TERMINATAR/POLYADENYLATION.USPT.	1
(L21 AND (TERMINAT$ SAME (SITE OR SIGNAL) SAME (DELETE$ OR MUTAT$ OR REMOV$ OR ELIMINAT$))).USPT.	39

There are more results than shown above. Click here to view the entire set.

Display Format: TI Change Format

Previous Page Next Page

WEST

Generate Collection | Print

Search Results - Record(s) 21 through 30 of 39 returned.

☐ 21. Document ID: US 5993799 A

L22: Entry 21 of 39 File: USPT Nov 30, 1999

US-PAT-NO: 5993799
DOCUMENT-IDENTIFIER: US 5993799 A

TITLE: Methods of using genetically engineered cells that produce insulin in response to glucose

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 22. Document ID: US 5958724 A

L22: Entry 22 of 39 File: USPT Sep 28, 1999

US-PAT-NO: 5958724
DOCUMENT-IDENTIFIER: US 5958724 A

TITLE: Process for producing heme proteins

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 23. Document ID: US 5879936 A

L22: Entry 23 of 39 File: USPT Mar 9, 1999

US-PAT-NO: 5879936
DOCUMENT-IDENTIFIER: US 5879936 A

TITLE: Recombinant DNA methods, vectors and host cells

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 24. Document ID: US 5837842 A

L22: Entry 24 of 39 File: USPT Nov 17, 1998

US-PAT-NO: 5837842
DOCUMENT-IDENTIFIER: US 5837842 A

TITLE: Vascular anticoagulant proteins DNA which codes them, processer for preparing them and their use

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 25. Document ID: US 5817495 A

L22: Entry 25 of 39 File: USPT Oct 6, 1998

US-PAT-NO: 5817495
DOCUMENT-IDENTIFIER: US 5817495 A

TITLE: H.sub.2 O.sub.2 -stable peroxidase variants

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 26. Document ID: US 5744323 A

L22: Entry 26 of 39 File: USPT Apr 28, 1998

US-PAT-NO: 5744323
DOCUMENT-IDENTIFIER: US 5744323 A

TITLE: Process for producing heme proteins

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 27. Document ID: US 5681725 A

L22: Entry 27 of 39 File: USPT Oct 28, 1997

US-PAT-NO: 5681725
DOCUMENT-IDENTIFIER: US 5681725 A

TITLE: Process for producing heme proteins

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 28. Document ID: US 5612190 A

L22: Entry 28 of 39 File: USPT Mar 18, 1997

US-PAT-NO: 5612190
DOCUMENT-IDENTIFIER: US 5612190 A

TITLE: DNA molecule encoding bovine group I phospholipase A.sub.2 receptor

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

29. Document ID: US 5585256 A

L22: Entry 29 of 39 File: USPT Dec 17, 1996

US-PAT-NO: 5585256
DOCUMENT-IDENTIFIER: US 5585256 A

TITLE: Aspergillus aculeatus rhamnogalacturon acetyl esterases, DNA sequences encoding the enzymes and methods of use thereof

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

30. Document ID: US 5486473 A

L22: Entry 30 of 39 File: USPT Jan 23, 1996

US-PAT-NO: 5486473
DOCUMENT-IDENTIFIER: US 5486473 A

TITLE: A DNA coding for a Flavivirus antigen

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

Generate Collection | Print

Term	Documents
SITE.USPT.	230237
SITES.USPT.	149027
SIGNAL.USPT.	833577
SIGNALS.USPT.	654885
TERMINAT$	0
TERMINAT.USPT.	22
TERMINATABILITY.USPT.	1
TERMINATABLE.USPT.	56
TERMINATAES.USPT.	3
TERMINATAL.USPT.	3
TERMINATAR/POLYADENYLATION.USPT.	1
(L21 AND (TERMINAT$ SAME (SITE OR SIGNAL) SAME (DELETE$ OR MUTAT$ OR REMOV$ OR ELIMINAT$))).USPT.	39

There are more results than shown above. Click here to view the entire set.

Display Format: TI Change Format

Previous Page Next Page

WEST

Generate Collection | Print

Search Results - Record(s) 31 through 39 of 39 returned.

☐ 31. Document ID: US 5374618 A

L22: Entry 31 of 39 File: USPT Dec 20, 1994

US-PAT-NO: 5374618
DOCUMENT-IDENTIFIER: US 5374618 A

TITLE: Calcitonin peptides, and gene related pharmaceutical compositions

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

☐ 32. Document ID: US 5332664 A

L22: Entry 32 of 39 File: USPT Jul 26, 1994

US-PAT-NO: 5332664
DOCUMENT-IDENTIFIER: US 5332664 A

TITLE: Human calcitonin precursor polyprotein structural gene

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

☐ 33. Document ID: US 5296467 A

L22: Entry 33 of 39 File: USPT Mar 22, 1994

US-PAT-NO: 5296467
DOCUMENT-IDENTIFIER: US 5296467 A

TITLE: Composition comprising an anticoagulant

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

☐ 34. Document ID: US 5296365 A

L22: Entry 34 of 39 File: USPT Mar 22, 1994

US-PAT-NO: 5296365
DOCUMENT-IDENTIFIER: US 5296365 A

TITLE: Production of guar alpha-galactosidase by hosts transformed with recombinant

DNA methods

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

---

☐ 35. Document ID: US 5240845 A

L22: Entry 35 of 39 File: USPT Aug 31, 1993

US-PAT-NO: 5240845
DOCUMENT-IDENTIFIER: US 5240845 A

TITLE: Mutated streptokinase proteins

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

---

☐ 36. Document ID: US 5210189 A

L22: Entry 36 of 39 File: USPT May 11, 1993

US-PAT-NO: 5210189
DOCUMENT-IDENTIFIER: US 5210189 A

TITLE: DNA sequence encoding glycerol 3-phosphate acyltransferase

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

---

☐ 37. Document ID: US 5175102 A

L22: Entry 37 of 39 File: USPT Dec 29, 1992

US-PAT-NO: 5175102
DOCUMENT-IDENTIFIER: US 5175102 A

TITLE: Modification of plant viruses or their effects

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWMC | Draw Desc | Image

---

☐ 38. Document ID: US 5136023 A

L22: Entry 38 of 39 File: USPT Aug 4, 1992

US-PAT-NO: 5136023
DOCUMENT-IDENTIFIER: US 5136023 A

TITLE: Polypeptide with cell-spreading activity

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

☐ 39. Document ID: US 5082778 A

L22: Entry 39 of 39 File: USPT Jan 21, 1992

US-PAT-NO: 5082778
DOCUMENT-IDENTIFIER: US 5082778 A

TITLE: Production of guar alpha-galactosidase by hosts transformed with recombinant DNA. methods

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Image | KWIC | Draw Desc

Generate Collection | Print

Term	Documents
SITE.USPT.	230237
SITES.USPT.	149027
SIGNAL.USPT.	833577
SIGNALS.USPT.	654885
TERMINAT$	0
TERMINAT.USPT.	22
TERMINATABILITY.USPT.	1
TERMINATABLE.USPT.	56
TERMINATAES.USPT.	3
TERMINATAL.USPT.	3
TERMINATAR/POLYADENYLATION.USPT.	1
(L21 AND (TERMINAT$ SAME (SITE OR SIGNAL) SAME (DELETE$ OR MUTAT$ OR REMOV$ OR ELIMINAT$))).USPT.	39

There are more results than shown above. Click here to view the entire set.

Display Format: TI Change Format

Previous Page Next Page

WEST

Generate Collection | Print

Search Results - Record(s) 11 through 12 of 12 returned.

☐ 11. Document ID: US 5089400 A

L25: Entry 11 of 12 File: USPT Feb 18, 1992

US-PAT-NO: 5089400
DOCUMENT-IDENTIFIER: US 5089400 A

TITLE: Polypeptides and process for the production thereof

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 12. Document ID: US 5004689 A

L25: Entry 12 of 12 File: USPT Apr 2, 1991

US-PAT-NO: 5004689
DOCUMENT-IDENTIFIER: US 5004689 A

TITLE: DNA sequences, recombinant DNA molecules and processes for producing human gamma interferon-like polypeptides in high yields

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

Generate Collection | Print

Term	Documents
ADDITION.USPT.	1604741
ADDN.USPT.	317
ADDNS.USPT.	15
ADDITIONS.USPT.	83072
POLY.USPT.	153988
POLIES.USPT.	6
POLYS.USPT.	105
A.USPT.	6579161
AS.USPT.	2402821
DELET$	0
DELET.USPT.	43
(L23 AND (ADDITION SAME (DELET$ OR MUTAT$ OR REMOV$ OR ELIMINAT$) SAME POLY ADJ "A")).USPT.	12

There are more results than shown above. Click here to view the entire set.

Display Format: TI Change Format

Previous Page Next Page

WEST

Help | Logout | Interrupt

Main Menu | Search Form | Posting Counts | Show S Numbers | Edit S Numbers | Preferences | Cases

Search Results -

Term	Documents
ADDITION.USPT.	1604741
ADDN.USPT.	317
ADDNS.USPT.	15
ADDITIONS.USPT.	83072
POLY.USPT.	153988
POLIES.USPT.	6
POLYS.USPT.	105
A.USPT.	6579161
AS.USPT.	2402821
DELET$	0
DELET.USPT.	43
(L23 AND (ADDITION SAME (DELET$ OR MUTAT$ OR REMOV$ OR ELIMINAT$) SAME POLY ADJ "A")).USPT.	12

There are more results than shown above. Click here to view the entire set.

Database: US Patents Full-Text Database
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
EPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search: L25

Refine Search

Recall Text | Clear

Search History

DATE: Monday, February 03, 2003 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT; PLUR=YES; OP=ADJ			
L25	L23 and (addition same (delet$ or mutat$ or remov$ or eliminat$) same poly adj "a")	12	L25
L24	L23 and (addition same (delet$ or mutat$ or remov$ or eliminat$))	144	L24
L23	l21 not l22	205	L23
L22	L21 and (terminat$ same (site or signal) same (delete$ or mutat$ or remov$ or eliminat$))	39	L22
L21	L17 not l20	244	L21
L20	L19 and ("aataaa" same (delet$ or modif$ or mutat$ or elimin$))	16	L20
L19	L17 and ("aataaa")	57	L19
L18	L17 and plant$	123	L18
L17	L16 and ((delet$ or mutat$ or remov$) same (signal or site))	260	L17
L16	L15 not l6	388	L16
L15	L14 not l12	398	L15
L14	(poly adj "a") same (terminat$ or polyadenyl$)and @PRAY<=1998	426	L14
L13	(poly adj "a") same (terminat$ or polyadenyl$)sa,e @PRAY<=1998	0	L13
L12	L8 and (signal same sequence same additi$5 same (poly adj "a"))	33	L12
L11	L8 and (signal same sequence same additi$5)	94	L11
L10	L9 and addition?	59	L10
L9	L8 and signal and sequence	274	L9
L8	L7 not l6	316	L8
L7	@PRAY <= 1998 AND (l4)	336	L7
L6	@PRAY <= 1999 AND (l5)	20	L6
L5	L4 and ((poly adj "a") same "gt")	74	L5
L4	(poly adj "a") and "gt" not l1	1896	L4
L3	(poly adj. "a") and "gt" not l1	0	L3
L2	(poly adj. "a") same "gt" not l1	0	L2
L1	"poly-a" same "gt"	11	L1

END OF SEARCH HISTORY